CLC **Sequence Viewer**

USER MANUAL

Manual for

CLC Sequence Viewer 7.6.1

Windows, Mac OS X and Linux

September 3, 2015

This software is for research purposes only.

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Part I

Introduction

Chapter 1

Introduction to *CLC Sequence Viewer*

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Welcome to *CLC Sequence Viewer 7.6.1* — a software package supporting your daily bioinformatics work.

We strongly encourage you to read this user manual in order to get the best possible basis for working with the software package.

This software is for research purposes only.

1.1 Contact information

The *CLC Sequence Viewer* is developed by:

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http://www.clcbio.com

VAT no.: DK 28 30 50 87

Telephone: 45 70 22 32 44
Fax: +45 86 20 12 22

E-mail: info@clcbio.com

If you have questions or comments regarding the program, you can contact us through the support team as described here: http://www.clcsupport.com/clcgenomicsworkbench/current/index.php?manual=Getting_help.html.

1.2 Download and installation

The *CLC Sequence Viewer* is developed for Windows, Mac OS X and Linux. The software for either platform can be downloaded from http://www.clcbio.com/download.

1.2.1 Program download

The program is available for download on http://www.clcbio.com/download.

Before you download the program you are asked to fill in the **Download** dialog.

In the dialog you must choose:

- Which operating system you use
- Whether you would like to receive information about future releases

Depending on your operating system and your Internet browser, you are taken through some download options.

When the download of the installer (an application which facilitates the installation of the program) is complete, follow the platform specific instructions below to complete the installation procedure.

1.2.2 Installation on Microsoft Windows

Starting the installation process is done in one of the following ways:

When you have downloaded an installer:
Locate the downloaded installer and double-click the icon.
The default location for downloaded files is your desktop.

Installing the program is done in the following steps:

- On the welcome screen, click **Next**.
- Read and accept the License agreement and click **Next**.
- Choose where you would like to install the application and click **Next**.
- Choose a name for the Start Menu folder used to launch *CLC Sequence Viewer* and click **Next**.
- Choose if *CLC Sequence Viewer* should be used to open CLC files and click **Next**.
- Choose where you would like to create shortcuts for launching *CLC Sequence Viewer* and click **Next**.
- Choose if you would like to associate .clc files to *CLC Sequence Viewer*. If you check this option, double-clicking a file with a "clc" extension will open the *CLC Sequence Viewer*.
- Wait for the installation process to complete, choose whether you would like to launch *CLC Sequence Viewer* right away, and click **Finish**.

When the installation is complete the program can be launched from the Start Menu or from one of the shortcuts you chose to create.

1.2.3 Installation on Mac OS X

Starting the installation process is done in the following way:

When you have downloaded an installer:
Locate the downloaded installer and double-click the icon.
The default location for downloaded files is your desktop.
Launch the installer by double-clicking on the "*CLC Sequence Viewer*" icon.

Installing the program is done in the following steps:

- On the welcome screen, click **Next**.
- Read and accept the License agreement and click **Next**.
- Choose where you would like to install the application and click **Next**.
- Choose if *CLC Sequence Viewer* should be used to open CLC files and click **Next**.
- Choose whether you would like to create desktop icon for launching *CLC Sequence Viewer* and click **Next**.
- Choose if you would like to associate .clc files to *CLC Sequence Viewer*. If you check this option, double-clicking a file with a "clc" extension will open the *CLC Sequence Viewer*.
- Wait for the installation process to complete, choose whether you would like to launch *CLC Sequence Viewer* right away, and click **Finish**.

When the installation is complete the program can be launched from your Applications folder, or from the desktop shortcut you chose to create. If you like, you can drag the application icon to the dock for easy access.

1.2.4 Installation on Linux with an installer

Navigate to the directory containing the installer and execute it. This can be done by running a command similar to:

```
# sh CLCSequenceViewer_7_6_1_64.sh.sh
```

Installing the program is done in the following steps:

- On the welcome screen, click **Next**.
- Read and accept the License agreement and click **Next**.
- Choose where you would like to install the application and click **Next**.
  For a system-wide installation you can choose for example /opt or /usr/local. If you do not have root privileges you can choose to install in your home directory.
- Choose where you would like to create symbolic links to the program
  DO NOT create symbolic links in the same location as the application.
  Symbolic links should be installed in a location which is included in your environment PATH. For a system-wide installation you can choose for example /usr/local/bin. If you do not have root privileges you can create a 'bin' directory in your home directory and install symbolic links there. You can also choose not to create symbolic links.
- Wait for the installation process to complete and click **Finish**.

If you choose to create symbolic links in a location which is included in your PATH, the program can be executed by running the command:

```
# clcseqview7
```

Otherwise you start the application by navigating to the location where you choose to install it and running the command:

```
# ./clcseqview7
```

1.2.5 Installation on Linux with an RPM-package

Navigate to the directory containing the rpm-package and install it using the rpm-tool by running a command similar to:

```
# rpm -ivh CLCSequenceViewer_7_6_1_64.sh.rpm
```

Installation of RPM-packages usually requires root-privileges.

When the installation process is finished the program can be executed by running the command:

```
# clcseqview7
```

1.3 System requirements

The system requirements of *CLC Sequence Viewer* are these:

- Windows Vista, Windows 7, Windows 8, or Windows Server 2008.
- Mac OS X 10.7 or later.
- Linux: RHEL 5.0 or later. SUSE 10.2 or later. Fedora 6 or later.
- 32 or 64 bit.
- 1 GB RAM required.
- 2 GB RAM recommended.
- 1024 x 768 display required.
- 1600 x 1200 display recommended. .

1.4 About CLC Workbenches

In November 2005 CLC bio released two Workbenches: *CLC Free Workbench* and *CLC Protein Workbench*. *CLC Protein Workbench* is developed from the free version, giving it the well-tested user friendliness and look & feel. However, the *CLC Protein Workbench* includes a range of more advanced analyses.

In March 2006, *CLC DNA Workbench* (formerly *CLC Gene Workbench*) and *CLC Main Workbench* were added to the product portfolio of CLC bio. Like *CLC Protein Workbench*, *CLC DNA Workbench* builds on *CLC Free Workbench*. It shares some of the advanced product features of *CLC Protein Workbench*, and it has additional advanced features. *CLC Main Workbench* holds all basic and advanced features of the *CLC Workbenches*.

In June 2007, *CLC RNA Workbench* was released as a sister product of *CLC Protein Workbench* and *CLC DNA Workbench*. *CLC Main Workbench* now also includes all the features of *CLC RNA Workbench*.

In March 2008, the *CLC Free Workbench* changed name to *CLC Sequence Viewer*.

In June 2008, the first version of the *CLC Genomics Workbench* was released due to an extraordinary demand for software capable of handling sequencing data from all new high-throughput sequencing platforms such as Roche-454, Illumina and SOLiD in addition to Sanger reads and hybrid data.

For an overview of which features all the applications include, see http://www.clcbio.com/features.

In December 2006, CLC bio released a **Software Developer Kit** which makes it possible for anybody with a knowledge of programming in Java to develop plugins. The plugins are fully integrated with the CLC Workbenches and the Viewer and provide an easy way to customize and extend their functionalities.

In April 2012, *CLC Protein Workbench*, *CLC DNA Workbench* and *CLC RNA Workbench* were discontinued. All customers with a valid license for any of these products were offered an upgrade to the *CLC Main Workbench*.

In February 2014, CLC bio expanded the product repertoire with the release of *CLC Drug Discovery Workbench*, a product that enables studies of protein-ligand interactions for drug discovery.

In April 2014, CLC bio released the *CLC Cancer Research Workbench*, a new product tailored to meet the requirements of clinicians and researchers working within the cancer field. The *Biomedical Genomics Workbench* contains streamlined data analysis workflows with integrated trimming and quality control.

In April 2015, the *CLC Cancer Research Workbench* was renamed to *Biomedical Genomics Workbench* to meet the requirements of clinicians and researchers working within the hereditary disease field, in addition to clinicians and researchers working within the cancer field.

1.4.1 New program feature request

The CLC team is continuously improving the *CLC Sequence Viewer* with our users' interests in mind. We welcome all requests and feedback from users, as well as suggestions for new features or more general improvements to the program. To contact us via the Workbench, please go to the menu option:

Help | **Contact Support**

1.4.2 Getting help

Users of the freely available CLC Sequence Viewer can make use of any of our online documentation sources, including the manuals (http://www.clcbio.com/manuals), tutorials (http://www.clcbio.com/tutorials) and other entries in our FAQ area (http://helpdesk.clcbio.com/index.php?pg=kb).

Start in safe mode

If the program becomes unstable on start-up, you can start it in **Safe mode**. This is done by pressing and holding down the Shift button while the program starts.

When starting in safe mode, the user settings (e.g. the settings in the **Side Panel**) are deleted and cannot be restored. Your data stored in the **Navigation Area** is not deleted. When started in safe mode, some of the functionalities are missing, and you will have to restart the *CLC Sequence Viewer* again (without pressing Shift.

1.4.3 CLC Sequence Viewer vs. Workbenches

The *CLC Sequence Viewer* is a user friendly application offering basic bioinformatics analyses. The *CLC Sequence Viewer* can be used to view outputs from many analyses of the CLC commercial workbenches, with notable exceptions being workflows and track-based data, which can only be viewed using our commercial Workbench offerings.

Track-based outputs can be viewed using the *CLC Genomics Workbench* and *CLC Main Workbench*, while workflows can be viewed in all commercial CLC workbenches, including the *CLC Main Workbench*, *CLC Genomics Workbench* and the *CLC Drug Discovery Workbench*.

The CLC Workbenches and the *CLC Sequence Viewer* are developed for Windows, Mac and Linux platforms. Data can be exported/imported between the different platforms in the same easy way

as when exporting/importing between two computers with e.g. Windows.

1.5 When the program is installed: Getting started

CLC Sequence Viewer includes an extensive **Help** function, which can be found in the **Help** menu of the program's **Menu bar**. The **Help** can also be shown by pressing F1. The help topics are sorted in a table of contents and the topics can be searched.

Tutorials describing hands-on examples of how to use the individual tools and features of the *CLC Sequence Viewer* can be found at http://www.clcbio.com/support/tutorials/. We also recommend our **Online presentations** where a product specialist from CLC bio demonstrates our software. This is a very easy way to get started using the program. Read more about video tutorials and other online presentations here: http://www.clcbio.tv/.

1.5.1 Quick start

When the program opens for the first time, the background of the workspace is visible. In the background are three quick start shortcuts, which will help you getting started. In the background are two quick start shortcuts, which will help you getting started. These can be seen in figure 1.1.

Figure 1.1: *Quick start short cuts, available in the background of the workspace.*

The function of the quick start shortcuts is explained here:

- **Import data.** Opens the **Import** dialog, which you let you browse for, and import data from your file system.
- **New sequence.** Opens a dialog which allows you to enter your own sequence.
- **Read tutorials.** Opens the tutorials menu with a number of tutorials. These are also available from the **Help** menu in the **Menu bar**.

Below these three quick start shortcuts, you will see a text: "Looking for more features?" Clicking this text will take you to a page on http://www.clcbio.com where you can read more about how to get more functionalities into *CLC Sequence Viewer*.

1.5.2 Import of example data

It might be easier to understand the logic of the program by trying to do simple operations on existing data. Therefore *CLC Sequence Viewer* includes an example data set.

When downloading *CLC Sequence Viewer* you are asked if you would like to import the example data set. If you accept, the data is downloaded automatically and saved in the program. If you didn't download the data, or for some other reason need to download the data again, you have two options:

You can click **Import Example Data** ( ) in the **Help** menu of the program. This imports the data automatically. You can also go to http://www.clcbio.com/download and download the example data from there.

If you download the file from the website, you need to import it into the program. See chapter 6 for more about importing data.

1.5.3 Import of example data

It might be easier to understand the logic of the program by trying to do simple operations on existing data. Therefore *CLC Sequence Viewer* includes an example data set.

If you would like to download the example data you have three options:

1. You can click **Download Example Data** in the start up table that is visible in the *CLC Sequence Viewer* when no datasets have been opened for viewing. This will take you to http://www.clcbio.com/support/downloads/#data where you can choose to download two different example datasets that can be used for the following purposes:
   - Variant identification in a tumor sample. This dataset is taken from a larger whole exome dataset and includes data from a small fraction of chromosome 5 (Example_data_tumor.zip).
   - Identification of somatic variants in a tumor sample using the matched normal sample for removal of germline variants. This is matched tumor and normal samples from chromosome 22 from a whole exome dataset (Example_data_tumor_normal.zip).
2. You can also go to directly to http://www.clcbio.com/support/downloads/#data and download the example data from there.
3. Finally, you can use these links to get the data:

   http://download.clcbio.com/testdata/cancer/current/Example_data_tumor.zip or

   http://download.clcbio.com/testdata/cancer/current/Example_data_tumor_normal.zip

When you have downloaded the data from the website, you need to import them into the *CLC Sequence Viewer*. How to import data is described in section 6.1.

1.6 Plugins

When you install *CLC Sequence Viewer*, it has a standard set of features. However, you can upgrade and customize the program using a variety of plugins.

As the range of plugins is continuously updated and expanded, they will not be listed here. Instead we refer to http://www.clcbio.com/plugins for a full list of plugins with descriptions of their functionalities.

1.6.1 Installing plugins

Plugins are installed using the plugin manager[1]:

Help in the Menu Bar | Plugins and Resources... ( )

or **Plugins ( ) in the Toolbar**

The plugin manager has three tabs at the top:

- **Manage Plugins.** This is an overview of plugins that are installed.
- **Download Plugins.** This is an overview of available plugins on CLC bio's server.
- **Manage Resources.** This is an overview of resources that are installed.

To install a plugin, click the **Download Plugins** tab. This will display an overview of the plugins that are available for download and installation (see figure 1.2).

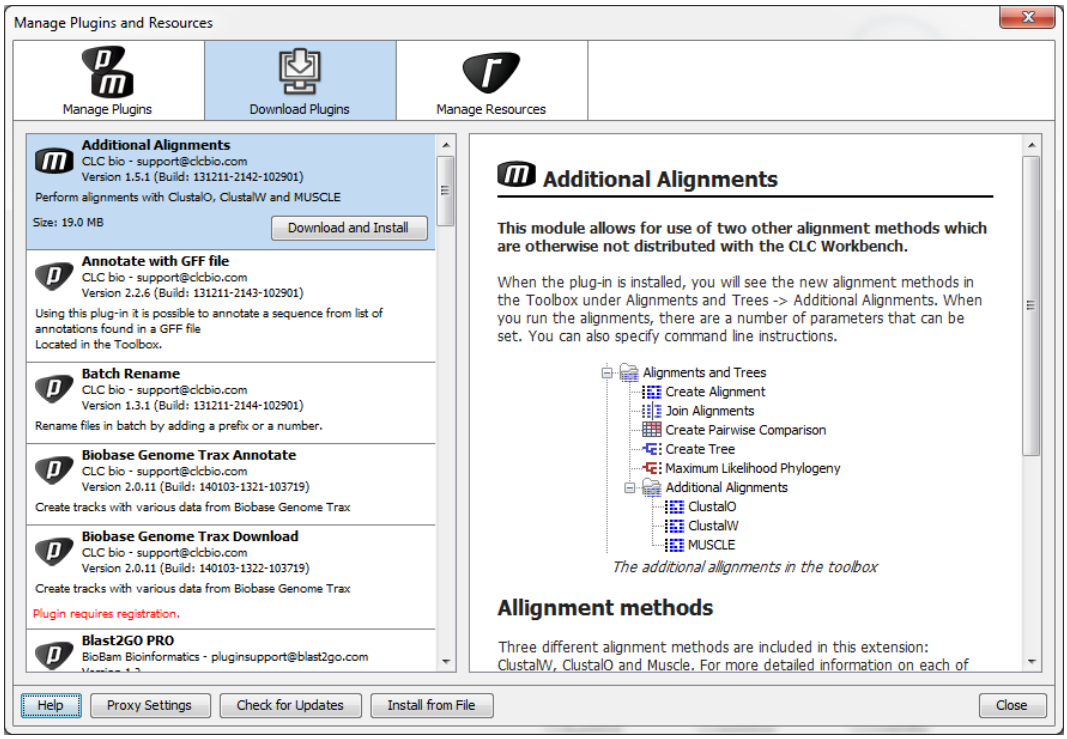
Manage Plugins and Resources
Manage Plugins
Download Plugins
Manage Resources
Additional Alignments
CLC bio - support@clcbio.com
Version 1.5.1 (Build: 131211-2142-102901)
Perform alignments with ClustalO, ClustalW and MUSCLE
Size: 19.0 MB
Download and Install
Annotate with GFF file
CLC bio - support@clcbio.com
Version 2.2.6 (Build: 131211-2143-102901)
Using this plug-in it is possible to annotate a sequence from list of annotations found in a GFF file
Located in the Toolbox.
Batch Rename
CLC bio - support@clcbio.com
Version 1.3.1 (Build: 131211-2144-102901)
Rename files in batch by adding a prefix or a number.
Biobase Genome Trax Annotate
CLC bio - support@clcbio.com
Version 2.0.11 (Build: 140103-1321-103719)
Create tracks with various data from Biobase Genome Trax
Biobase Genome Trax Download
CLC bio - support@clcbio.com
Version 2.0.11 (Build: 140103-1322-103719)
Create tracks with various data from Biobase Genome Trax
Plugin requires registration.
Blast2GO PRO
BioBam Bioinformatics - pluginsupport@blast2go.com
Additional Alignments
This module allows for use of two other alignment methods which are otherwise not distributed with the CLC Workbench.
When the plug-in is installed, you will see the new alignment methods in the Toolbox under Alignments and Trees -> Additional Alignments. When you run the alignments, there are a number of parameters that can be set. You can also specify command line instructions.
Alignments and Trees
Create Alignment
Join Alignments
Create Pairwise Comparison
Create Tree
Maximum Likelihood Phylogeny
Additional Alignments
ClustalO
ClustalW
MUSCLE
The additional allignments in the toolbox
Allignment methods
Three different alignment methods are included in this extension:
ClustalW, ClustalO and Muscle. For more detailed information on each of
Help
Proxy Settings
Check for Updates
Install from File
Close

Figure 1.2: *The plugins that are available for download.*

Clicking a plugin will display additional information at the right side of the dialog. This will also display a button: **Download and Install**.

Click the plugin and press **Download and Install**. A dialog displaying progress is now shown, and the plugin is downloaded and installed.

If the plugin is not shown on the server, and you have it on your computer (e.g. if you have downloaded it from our web-site), you can install it by clicking the **Install from File** button at the

[1] In order to install plugins on Windows, the Workbench must be run in administrator mode: Right-click the program shortcut and choose "Run as Administrator". Then follow the procedure described below.

bottom of the dialog. This will open a dialog where you can browse for the plugin. The plugin file should be a file of the type ".cpa".

When you close the dialog, you will be asked whether you wish to restart the *CLC Sequence Viewer*. The plugin will not be ready for use until you have restarted.

1.6.2 Uninstalling plugins

Plugins are uninstalled using the plugin manager:

Help in the Menu Bar | **Plugins and Resources... ( )**

or **Plugins ( ) in the Toolbar**

This will open the dialog shown in figure 1.3.

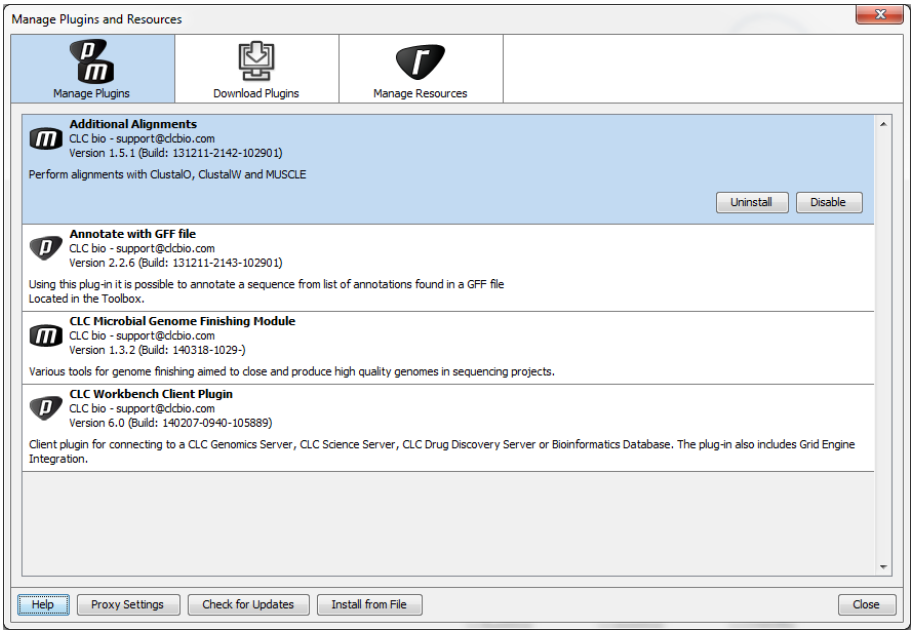
Manage Plugins and Resources
Manage Plugins
Download Plugins
Manage Resources
Additional Alignments
CLC bio - support@clcbio.com
Version 1.5.1 (Build: 131211-2142-102901)
Perform alignments with ClustalO, ClustalW and MUSCLE
Uninstall
Disable
Annotate with GFF file
CLC bio - support@clcbio.com
Version 2.2.6 (Build: 131211-2143-102901)
Using this plug-in it is possible to annotate a sequence from list of annotations found in a GFF file Located in the Toolbox.
CLC Microbial Genome Finishing Module
CLC bio - support@clcbio.com
Version 1.3.2 (Build: 140318-1029-)
Various tools for genome finishing aimed to close and produce high quality genomes in sequencing projects.
CLC Workbench Client Plugin
CLC bio - support@clcbio.com
Version 6.0 (Build: 140207-0940-105889)
Client plugin for connecting to a CLC Genomics Server, CLC Science Server, CLC Drug Discovery Server or Bioinformatics Database. The plug-in also includes Grid Engine Integration.
Help
Proxy Settings
Check for Updates
Install from File
Close

Figure 1.3: *The plugin manager with plugins installed.*

The installed plugins are shown in this dialog. To uninstall:

Click the plugin | **Uninstall**

If you do not wish to completely uninstall the plugin but you don't want it to be used next time you start the Workbench, click the **Disable** button.

When you close the dialog, you will be asked whether you wish to restart the workbench. The plugin will not be uninstalled until the workbench is restarted.

1.6.3 Updating plugins

If a new version of a plugin is available, you will get a notification during start-up as shown in figure 1.4.

In this list, select which plugins you wish to update, and click **Install Updates**. If you press **Cancel** you will be able to install the plugins later by clicking **Check for Updates** in the Plugin

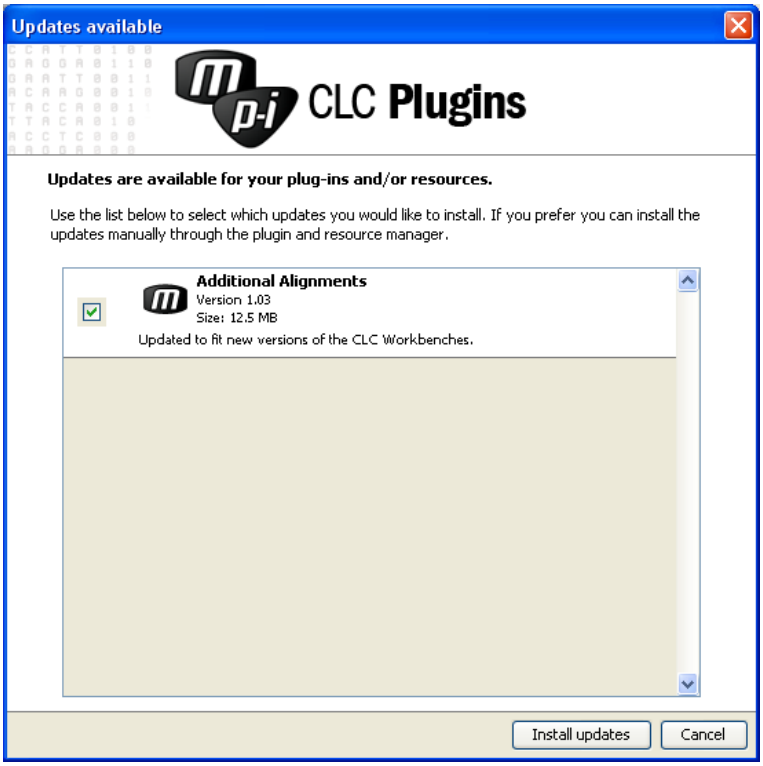
Updates available
CLC Plugins
Updates are available for your plug-ins and/or resources.
Use the list below to select which updates you would like to install. If you prefer you can install the updates manually through the plugin and resource manager.
Additional Alignments
Version 1.03
Size: 12.5 MB
Updated to fit new versions of the CLC Workbenches.
Install updates
Cancel

Figure 1.4: *Plugin updates.*

manager (see figure 1.3).

1.6.4 Resources

Resources can be manually installed and un-installed the same way as plugins.

1.7 Network configuration

If you use a proxy server to access the Internet you must configure *CLC Sequence Viewer* to use this. Otherwise you will not be able to perform any online activities (e.g. searching GenBank).

CLC Sequence Viewer supports the use of an HTTP-proxy and an anonymous SOCKS-proxy.

To configure your proxy settings, open *CLC Sequence Viewer*, and go to the **Advanced**-tab of the **Preferences** dialog (figure 1.5) and enter the appropriate information. The **Preferences** dialog is opened from the **Edit** menu.

You have the choice between an HTTP-proxy and a SOCKS-proxy. *CLC Sequence Viewer* only supports the use of a SOCKS-proxy that does not require authorization.

You can select whether the proxy should be used also for FTP and HTTPS connections.

Exclude hosts can be used if there are some hosts that should be contacted directly and not through the proxy server. The value can be a list of hosts, each separated by a `|`, and in addition a wildcard character `*` can be used for matching. For example: `*.foo.com|localhost`.

If you have any problems with these settings you should contact your systems administrator.

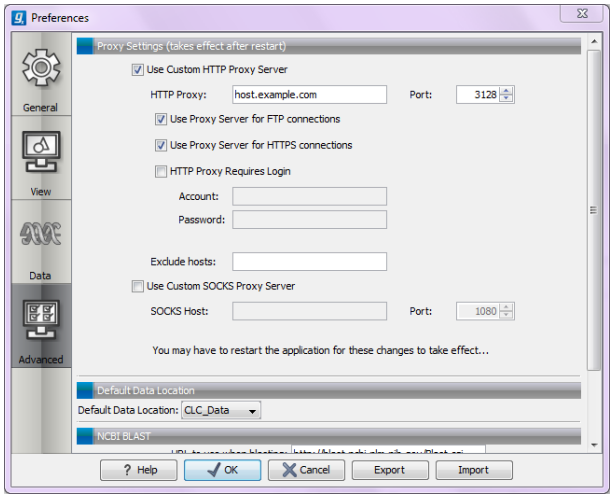

Figure 1.5: *Adjusting proxy preferences.*

1.8 The format of the user manual

This user manual offers support to Windows, Mac OS X and Linux users. The software is very similar on these operating systems. In areas where differences exist, these will be described separately. However, the term "right-click" is used throughout the manual, but some Mac users may have to use Ctrl+click in order to perform a "right-click" (if they have a single-button mouse).

The most recent version of the user manuals can be downloaded from `http://www.clcbio.com/usermanuals`.

The user manual consists of four parts.

- The **first part** includes the introduction to the *CLC Sequence Viewer*.
- The **second part** describes in detail how to operate all the program's basic functionalities.
- The **third part** digs deeper into some of the molecular modeling and bioinformatic features of the program. In this part, you will also find our "Bioinformatics explained" sections. These sections elaborate on the algorithms and analyses of *CLC Sequence Viewer* and provide more general knowledge of molecular modeling and bioinformatic concepts.
- The **fourth part** is the Appendix and Index.

Each chapter includes a short table of contents.

1.8.1 Text formats

In order to produce a clearly laid-out content in this manual, different formats are applied:

- A feature in the program is in bold starting with capital letters. (Example: **Navigation Area**)
- An explanation of how a particular function is activated, is illustrated by "|" and bold. (E.g.: **select the element** | **Edit** | **Rename**)

1.9 Latest improvements

CLC Sequence Viewer is under constant development and improvement. A detailed list that includes a description of new features, improvements, bugfixes, and changes for the current version of *CLC Sequence Viewer* can be found at:

http://www.clcbio.com/products/latest-improvements-sequence-viewer/

Chapter 2

Tutorials

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This chapter contains tutorials representing some of the features of *CLC Sequence Viewer*. The first tutorials are meant as a short introduction to operating the program. The last tutorials give examples of how to use some of the main features of *CLC Sequence Viewer*. **Watch video tutorials at `http://www.clcbio.tv`.**

2.1 Tutorial: Getting Started

This brief tutorial will take you through the most basic steps of working with the CLC Workbenches. The tutorial introduces the user interface, shows how to create a folder, and demonstrates how to import your own existing data into the program. The *CLC Sequence Viewer* will be used to illustrate these functions.

When you open *CLC Sequence Viewer* for the first time, the user interface looks like figure 2.1.

At this stage, the important issues are the **Navigation Area** and the **View Area**.

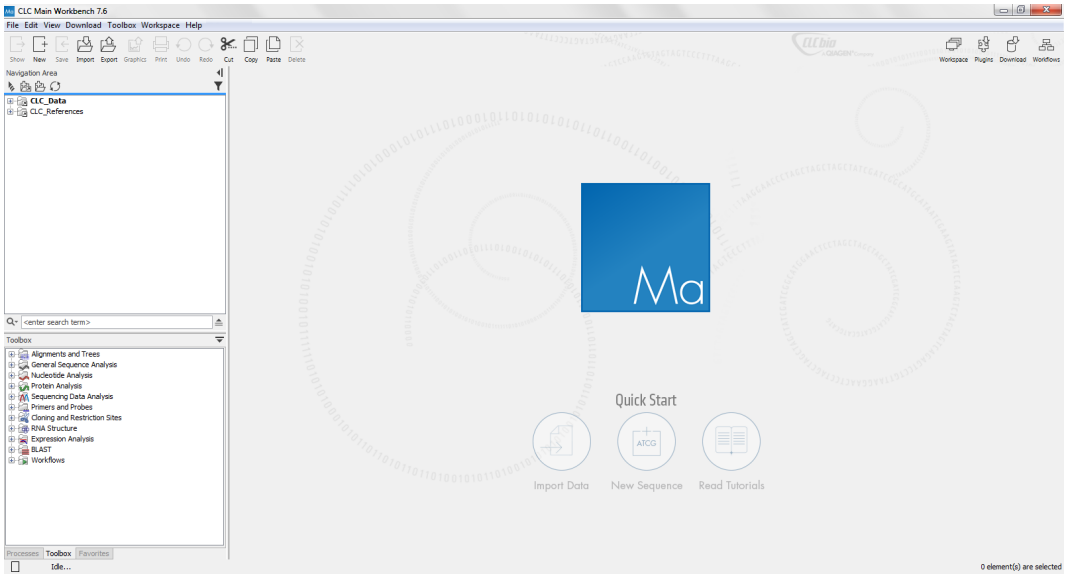

Figure 2.1: *The user interface as it looks when you start the program for the first time. (Mac version of* **CLC Sequence Viewer***. The interface is similar for Windows and Linux.)*

The **Navigation Area** to the left is where you keep all your data for use in the program. Most analyses of *CLC Sequence Viewer* require that the data is saved in the **Navigation Area**. There are several ways to get data into the **Navigation Area**, and this tutorial describes how to import existing data.

The **View Area** is the main area to the right. This is where the data can be 'viewed'. In general, a **View** is a display of a piece of data, and the **View Area** can include several **Views**. The **Views** are represented by tabs, and can be organized e.g. by using 'drag and drop'.

2.1.1 Creating a a folder

When *CLC Sequence Viewer* is started there is one element in the **Navigation Area** called **CLC_Data**[1]. This element is a **Location**. A location points to a folder on your computer where your data for use with *CLC Sequence Viewer* is stored.

The data in the location can be organized into folders. Create a folder:

File | New | Folder ( )
or **Ctrl + Shift + N (⌘ + Shift + N on Mac)**

Name the folder 'My folder' and press **Enter**.

2.1.2 Import data

As an example, first generation sequence data as well as high throughput sequencing data can be downloaded from `http://www.clcbio.com/downloads` under "EXAMPLE DATA", Roche/454 pyrosequencing genome data from E. coli commensal strain K-12. The NC_010473.gbk (GenBank format) can be imported by all types of CLC Workbenches, while import of the high throughput sequencing data requires specialised import actions. (This "EXAMPLE DATA" file is chosen for demonstration purposes only - you may have another file on your desktop,

[1] If you have downloaded the example data, this will be placed as a folder in *CLC_Data*

which you can use to follow this tutorial. You can import all kinds of files.)

The sequence data is imported into the folder that was selected in the **Navigation Area**, before you clicked **Import**. Double-click the sequence in the **Navigation Area** to view it. The NC_010473.gbk (GenBank format) result looks like figure 2.2 while the high throughput data looks like figure 2.3.

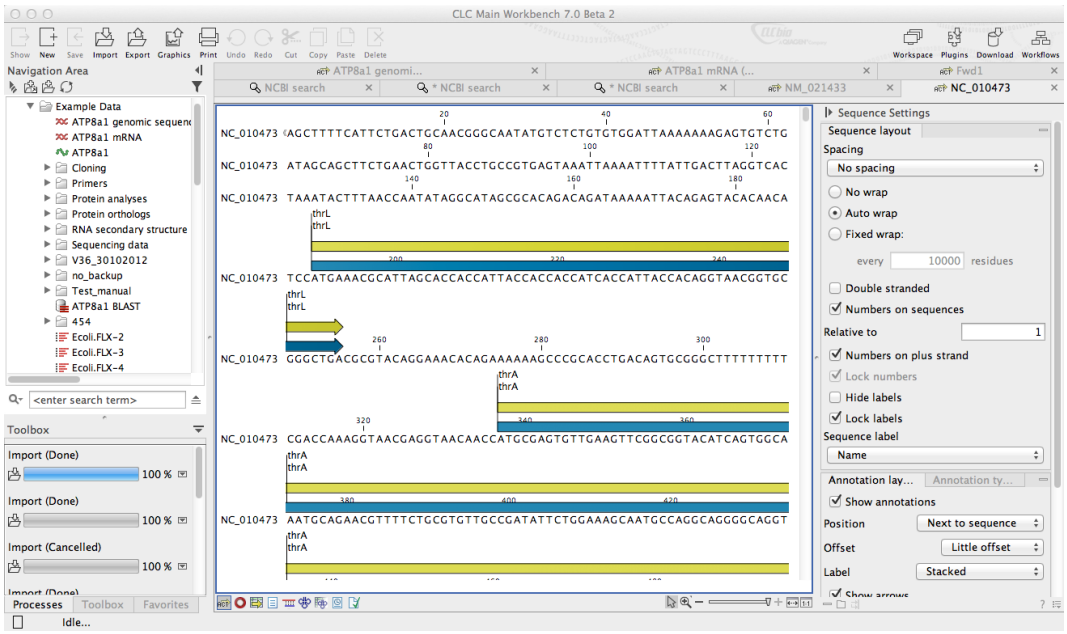

Figure 2.2: *The NC_010473.gbk (GenBank format) file is imported and opened.*

The sequence is imported into the folder that was selected in the **Navigation Area**, before you clicked **Import**. Double-click the sequence in the **Navigation Area** to view it.

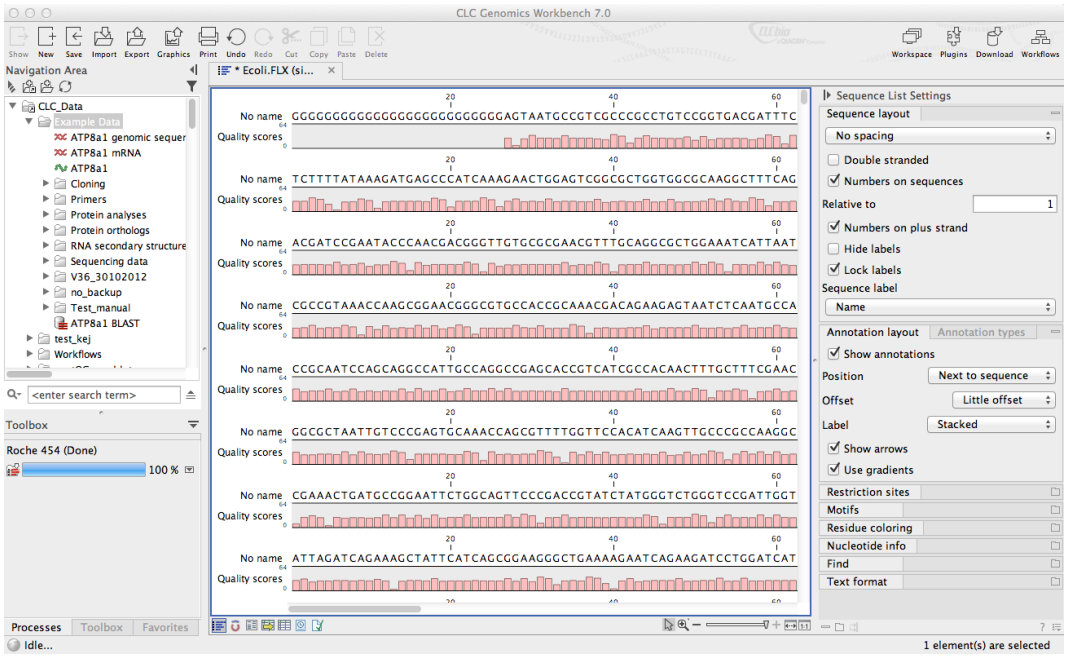

Figure 2.3: *The NC_010473 high throughput data imported and opened.*

2.2 Tutorial: View a DNA Sequence

This brief tutorial will take you through some different ways to display a sequence in the program. The tutorial introduces zooming on a sequence, dragging tabs, and opening selection in new view.

We will be working with the sequence called *pcDNA3-atp8a1* located in the 'Cloning' folder in the Example data. Double-click the sequence in the **Navigation Area** to open it. The sequence is displayed with annotations above it. (See figure 2.4).

Figure 2.4: *Sequence pcDNA3-atp8a1 opened in a view.*

As default, *CLC Sequence Viewer* displays a sequence with annotations (colored arrows on the sequence like the green promoter region annotation in figure 2.4) and zoomed to see the residues.

In this tutorial we want to have an overview of the whole sequence. Hence;

> **click Zoom Out ( ) in the Toolbar | click the sequence until you can see the whole sequence**

This sequence is circular, which is indicated by << and >> at the beginning and the end of the sequence.

In the following we will show how the same sequence can be displayed in two different views - one linear view and one circular view. First, zoom in to see the residues again by using the **Zoom In** ( ) or the **100%** ( ). Then we make a split view by:

> **press and hold the Ctrl-button on the keyboard (⌘ on Mac) | click Show as Circular ( ) at the bottom of the view**

This opens an additional view of the vector with a circular display, as can be seen in figure 2.5.

You may want to change the text size in the top panel to see more of the sequence. Scroll down in the **Sequence Settings** panel to **Text format** and change text size to **Tiny** or **Small**. You can also resize the panels relative to each other by clicking and dragging the separator line between

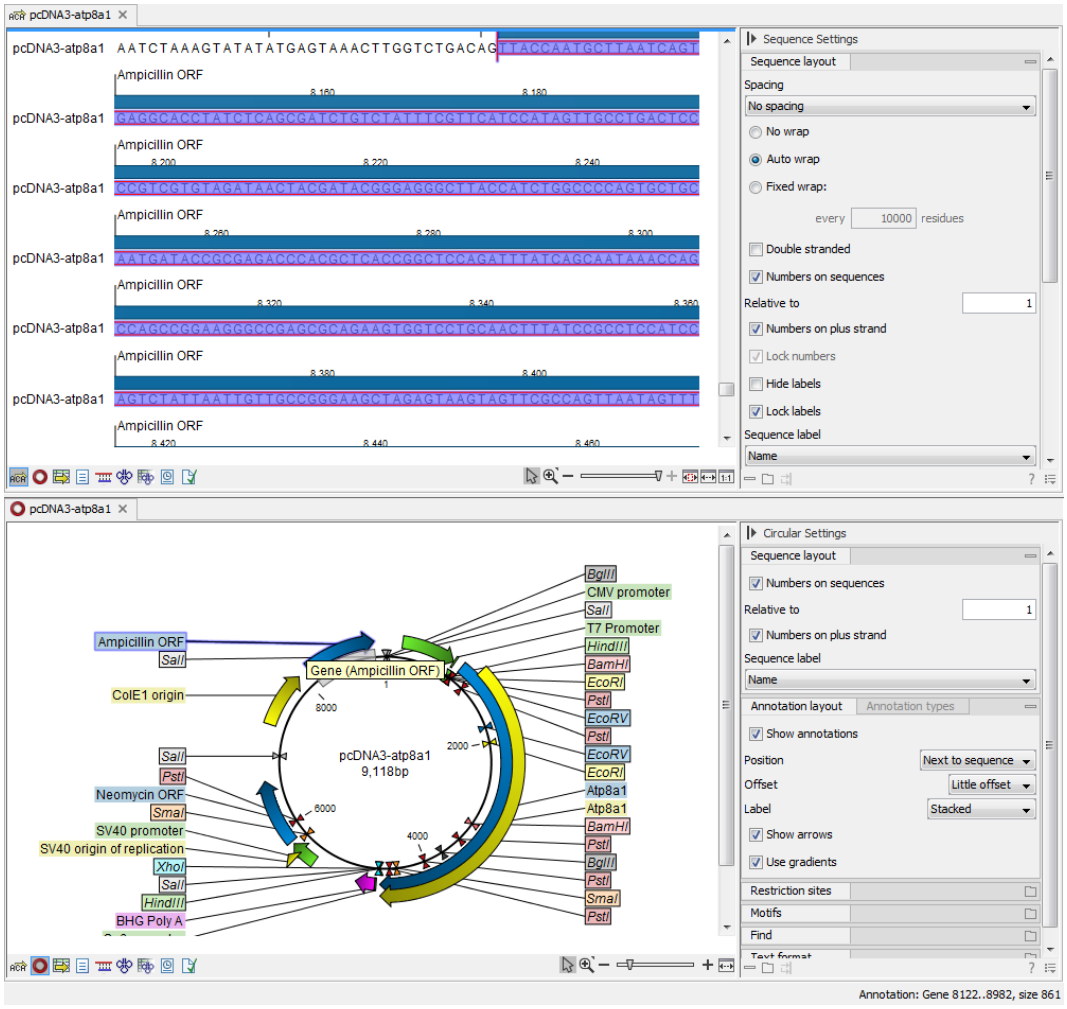

Figure 2.5: *The resulting two views which are split horizontally.*

them.

Make a selection on the circular sequence (remember to switch to the **Selection** ( ) tool in the tool bar). Note that this selection is also reflected in the linear view above, and that the selection coordinates appear at the bottom right corner of the screen (in figure 2.5 the **Ampicillin ORF** was selected).

You can open a third view of just the selected part of the sequence by right-clicking anywhere in the highlighted sequence text in the top panel and choosing **Open Selection in New View** as shown in figure 2.6.

Click and drag the new tab from the bottom panel to the top one, next to the existing linear view.

2.3 Tutorial: Side Panel Settings

This brief tutorial will show you how to use the **Side Panel** to change the way your sequences, alignments and other data are shown. You will also see how to save the changes that you made in the **Side Panel** .

Open the protein alignment located under *Protein orthologs* in the **Example data**. The initial

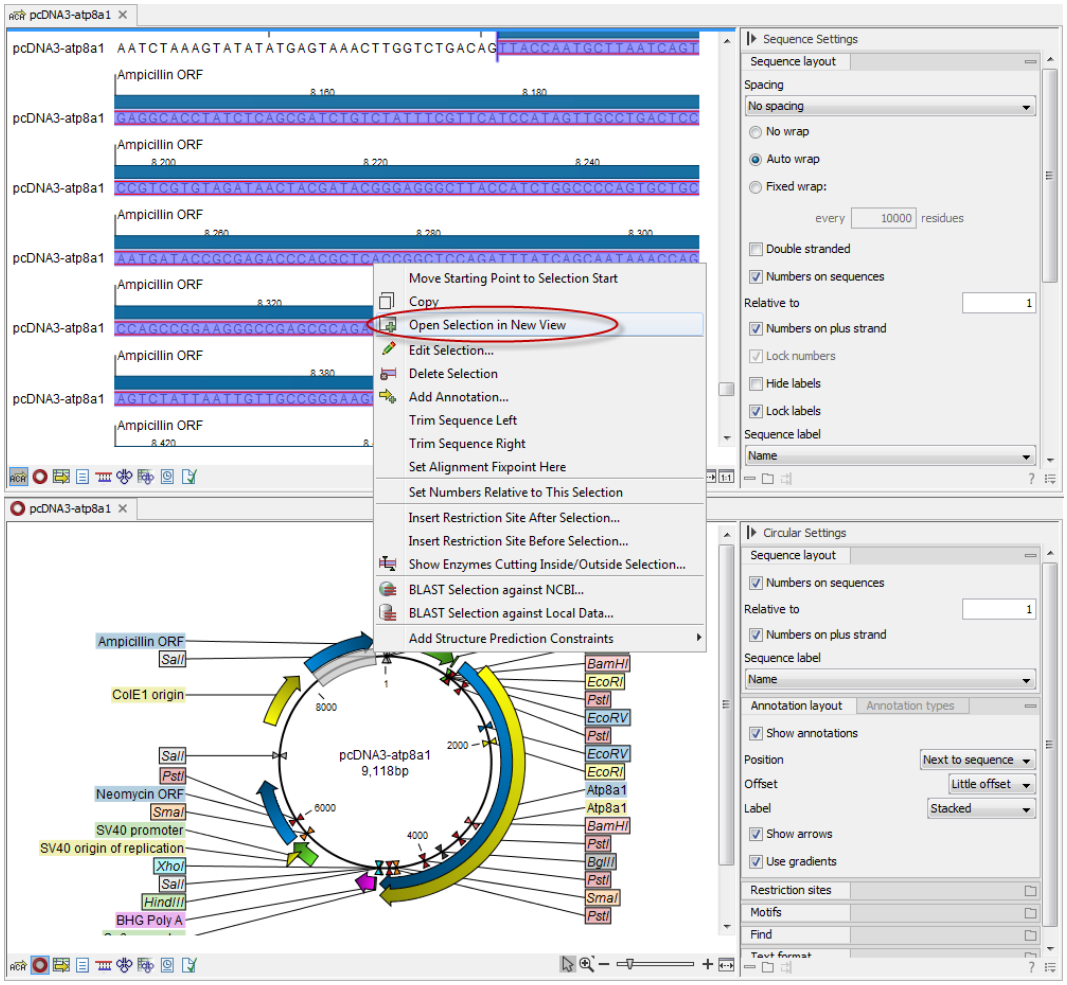

Figure 2.6: *Creating a new view panel for just the selected sequence.*

view of the alignment has colored the residues according to the Rasmol color scheme, and the alignment is automatically wrapped to fit the width of the view (shown in figure 2.7).

Now, we are going to modify how this alignment is displayed. For this, we use the settings in the **Side Panel** to the right. All the settings are organized into groups, which can be expanded / collapsed by clicking the name of the group. The first group is **Sequence Layout** which is expanded by default.

First, select **No wrap** in the **Sequence Layout**. This means that each sequence in the alignment is kept on the same line. To see more of the alignment, you now have to scroll horizontally.

Next, expand the **Annotation Layout** group and select **Show Annotations**. Set the **Offset** to "More offset" and set the **Label** to "Stacked".

Click on the **Annotation Types** tab. Here you will see a list of the types annotation that are carried by the sequences in the alignment (see figure 2.8).

Check the "Region" annotation type, and you will see the regions as red annotations on the sequences.

Next, we will change the way the residues are colored. Click the **Alignment Info** group and under **Conservation**, check "Background color". This will use a gradient as background color for the

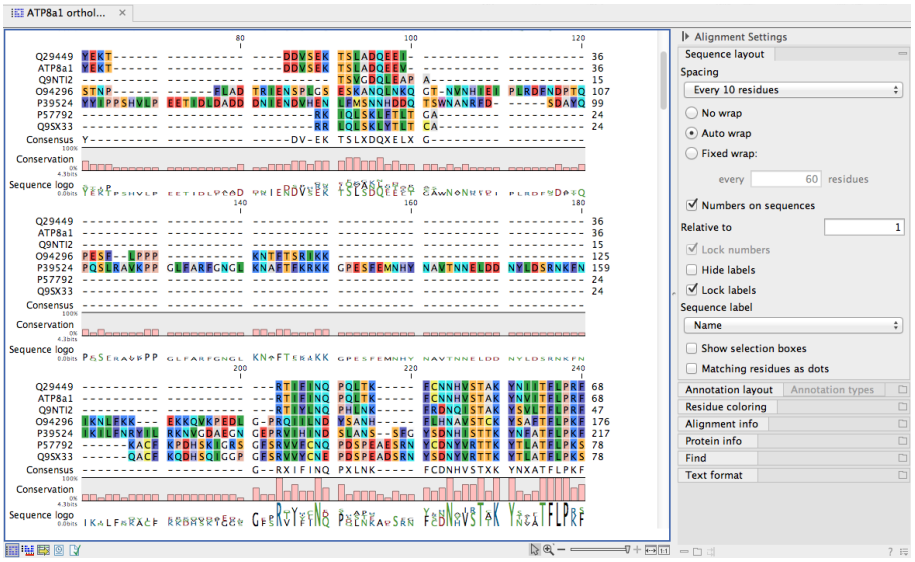

Figure 2.7: *The protein alignment as it looks when you open it with background color according to the Rasmol color scheme and automatically wrapped.*

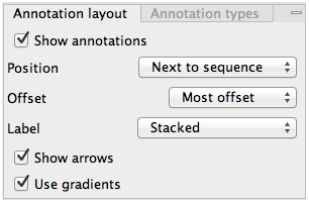

Figure 2.8: *The Annotation Layout and the Annotation Types tabs in the Side Panel.*

residues. You can adjust the coloring by dragging the small arrows above the color box.

2.3.1 Saving the settings in the Side Panel

Now the alignment should look similar to figure 2.9.

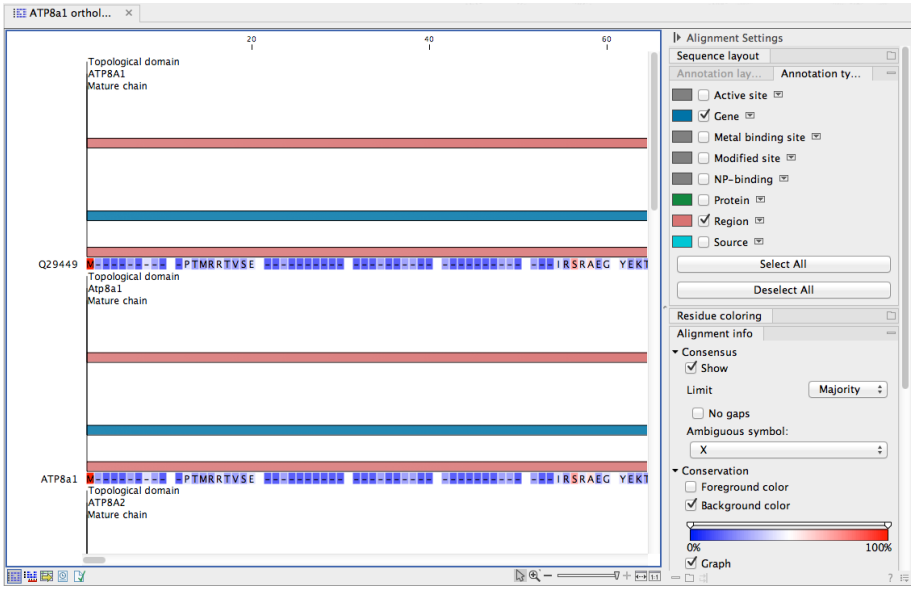

Figure 2.9: *The alignment when all the above settings have been changed.*

At this point, if you just close the view, the changes made to the **Side Panel** will not be saved. This means that you would have to perform the changes again next time you open the alignment. To save the changes to the **Side Panel**, click the **Save/Restore Settings** button ( ) at the bottom of the **Side Panel** and click **Save Alignment View Settings** (see figure 2.10).

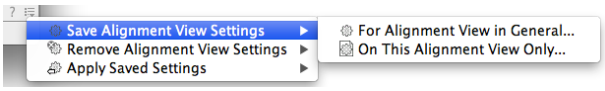
Save Alignment View Settings
Remove Alignment View Settings
Apply Saved Settings
For Alignment View in General...
On This Alignment View Only...

Figure 2.10: *Saving the settings of the Side Panel either generally or this particular alignment only.*

This will open the dialog shown in figure 2.11.

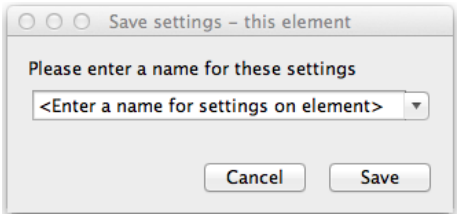

Figure 2.11: *Dialog for saving the settings of the Side Panel.*

In this way you can save the current state of the settings in the **Side Panel** so that you can apply them to alignments later on. If you check **Always apply these settings**, these settings will be applied every time you open a view of the alignment.

Type "My settings" in the dialog and click **Save**.

2.3.2 Remove alignment view settings

When you click the **Save/Restore Settings** button ( ) and select **Remove Alignments View Settings**, you can choose whether this should be applied generally or on this alignment view only (see figure 2.12).

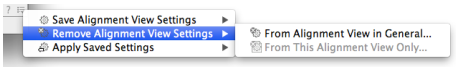
Save Alignment View Settings
Remove Alignment View Settings
Apply Saved Settings
From Alignment View in General...
From This Alignment View Only...

Figure 2.12: *Menu for removing saved settings.*

This will open the dialog shown in figure 2.13 and allow you to remove specific settings.

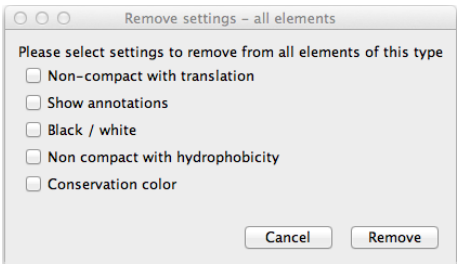

Figure 2.13: *Menu for removing saved settings.*

2.3.3 Applying saved settings

When you click the **Save/Restore Settings** button ( ) again and select **Apply Saved Settings**, you will see "My settings" in the menu together with some pre-defined settings that the *CLC*

Sequence Viewer has created for you (see figure 2.14).

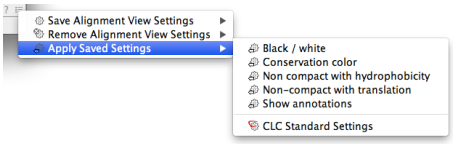

Figure 2.14: *Menu for applying saved settings.*

Whenever you open an alignment, you will be able to apply these settings. Each kind of view has its own list of settings that can be applied.

At the bottom of the list you will see the "CLC Standard Settings" which are the default settings for the view.

2.4 Tutorial: Align Protein Sequences

This tutorial outlines some of the alignment functionality of the *CLC Sequence Viewer*. In addition to creating alignments of nucleotide or peptide sequences, the software offers several ways to view alignments. The alignments can then be used for building phylogenetic trees.

Sequences must be available via the **Navigation Area** to be included in an alignment. If you have sequences open in a View that you have not saved, then you just need to select the view tab and press Ctrl + S (or ⌘ + S on Mac) to save them.

In this tutorial six protein sequences from the Example data folder will be aligned. (See figure 2.15).

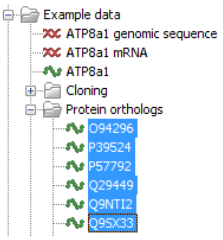

Figure 2.15: *Six protein sequences in 'Sequences' from the 'Protein orthologs' folder of the Example data.*

To align the sequences:

> **select and then right click on the sequences from the 'Protein orthologs' folder under 'Example Data' | Toolbox | Alignments and Trees ( )| Create Alignment ( )**

2.4.1 The alignment dialog

This opens the dialog shown in figure 2.16.

It is possible to add and remove sequences from **Selected Elements** list. Since we had already selected the six proteins, just click **Next** to adjust parameters for the alignment.

Clicking **Next** opens the dialog shown in figure 2.17.

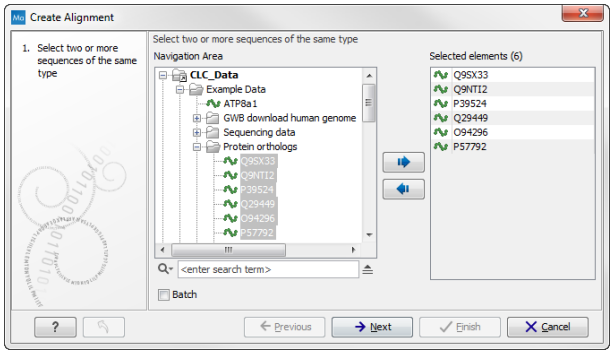

Figure 2.16: *The alignment dialog displaying the six protein sequences.*

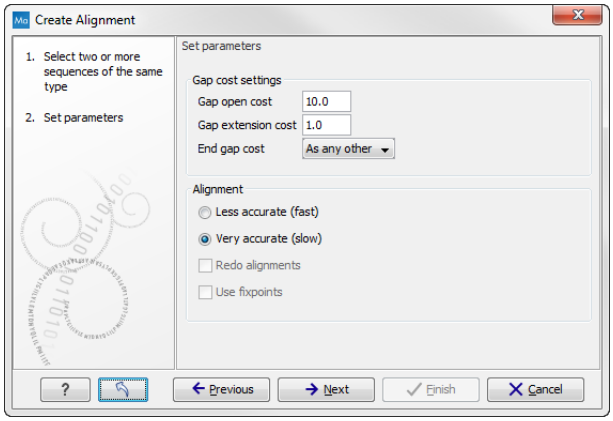

Figure 2.17: *The alignment dialog displaying the available parameters which can be adjusted.*

Leave the parameters at their default settings. An explanation of the parameters can be found by clicking the help button (?). Alternatively, a tooltip is displayed by holding the mouse cursor on the parameters.

Click on the button labeled **Next** and specify where you would like to save the data. Click on the button labeled **Finish** to start the alignment process which is shown in the **Toolbox** under the **Processes** tab. When the program is finished calculating it displays the alignment (see fig. 2.18):

Open the generated output from the destination where you choose to save it. Alternatively, the output can be opened by clicking on the small arrow next to the process bar and choosing **Find Results** as shown in figure 2.19):

Installing the Additional Alignments plugin gives you access to two other alignment algorithms: ClustalW (Windows/Mac/Linux) and Muscle (Windows/Mac/Linux). The Additional Alignments Module can be downloaded from `http://www.clcbio.com/plugins`. Note that you will need administrative privileges on your system to install it.

2.5 Tutorial: Find Restriction Sites

This tutorial will show you how to find restriction sites and annotate them on a sequence.

There are two ways of finding and showing restriction sites. In many cases, the dynamic restriction sites found in the **Side Panel** of sequence views will be useful, since it is a quick and easy way of showing restriction sites. In the **Toolbox** you will find the other way of doing restriction site

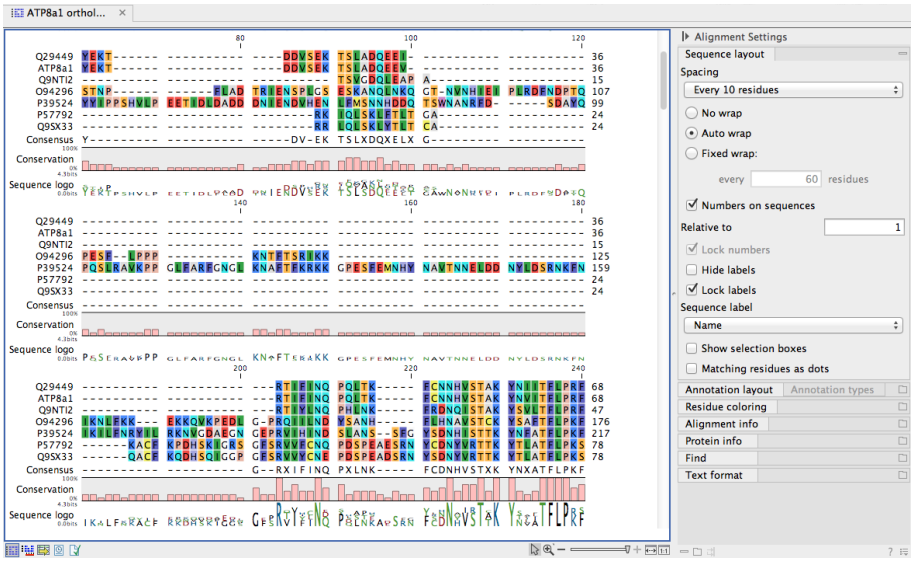

Figure 2.18: *The resulting alignment.*

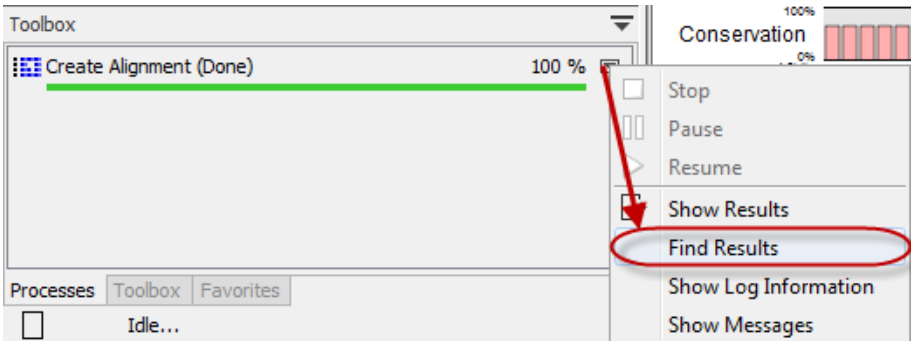

Figure 2.19: *Find and open the output that was generated.*

analyses. This way provides more control of the analysis and gives you more output options, e.g. a table of restriction sites and a list of restriction enzymes that can be saved for later use. In this tutorial, the first section describes how to use the Side Panel to show restriction sites, whereas the second section describes the restriction map analysis performed from the **Toolbox**.

2.5.1 The Side Panel way of finding restriction sites

When you open a sequence, there is a **Restriction sites** setting in the **Side Panel**. By default, 10 of the most popular restriction enzymes are shown (see figure 2.20).

The restriction sites are shown on the sequence with an indication of cut site and recognition sequence. In the list of enzymes in the **Side Panel**, the number of cut sites is shown in parentheses for each enzyme (e.g. *SalI* cuts three times). If you wish to see the recognition sequence of the enzyme, place your mouse cursor on the enzyme in the list for a short moment, and a tool tip will appear.

You can add or remove enzymes from the list by clicking the **Manage enzymes** button.

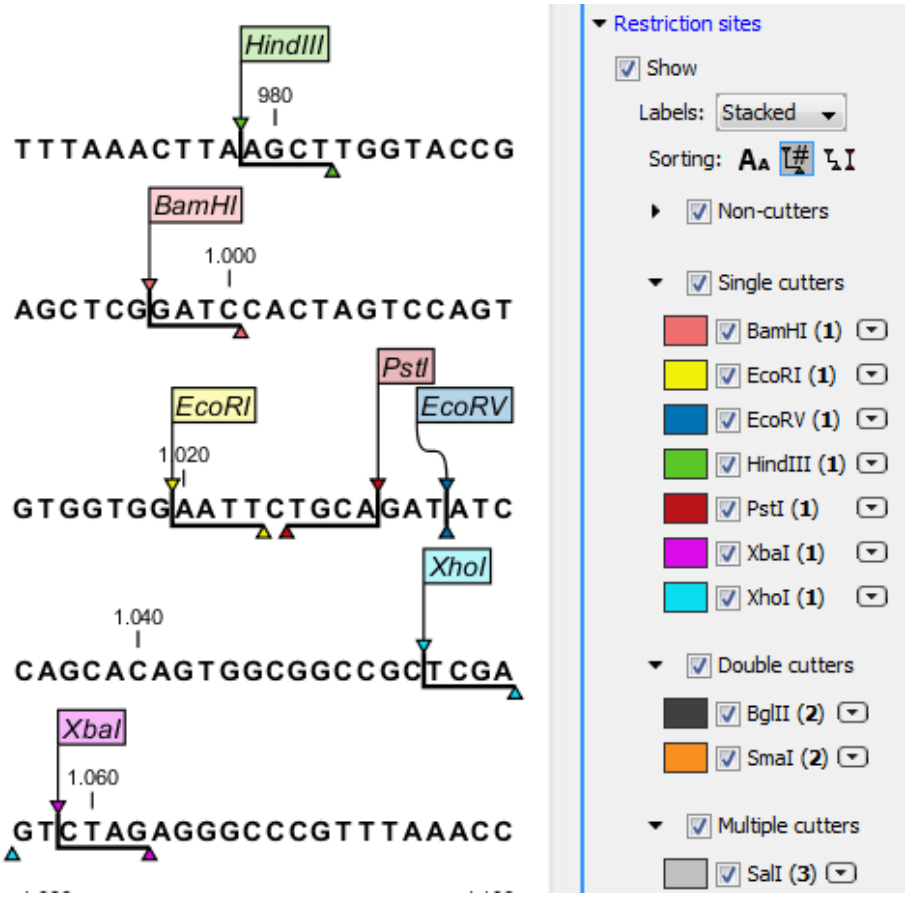

Figure 2.20: *Showing restriction sites of ten restriction enzymes.*

2.5.2 The Toolbox way of finding restriction sites

Suppose you are working with sequence 'ATP8a1 mRNA' from the example data, and you wish to know which restriction enzymes will cut this sequence exactly once and create a 3' overhang. Do the following:

> **select the ATP8a1 mRNA | Toolbox in the Menu Bar | Restriction Sites ( ) | Restriction Site Analysis ( )**

Click **Next** to set parameters for the restriction map analysis.

In this step first select **Use existing enzyme list** and click the **Browse for enzyme list** button ( ). Select the 'Popular enzymes' in the Cloning folder under Enzyme lists (figure 2.21).

Then write 3' into the filter below to the left. Select all the enzymes and click the **Add** button ( ). The result should be like in figure 2.22.

Click on the button labeled **Next**. In this step you specify that you want to show enzymes that cut the sequence only once. This means that you should de-select the **Two restriction sites** checkbox (See figure 2.23).

Click on the button labeled **Next** and select that you want to **Add restriction sites as annotations on sequence** and **Create restriction map** (figure 2.24).

Click on the button labeled **Finish** to start the restriction map analysis.

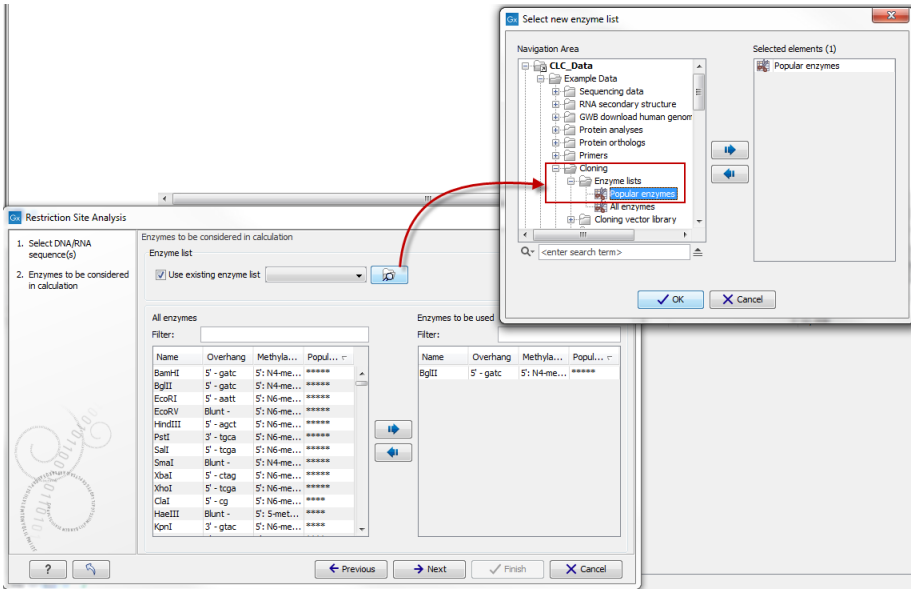

Figure 2.21: *Selecting enzyme list.*

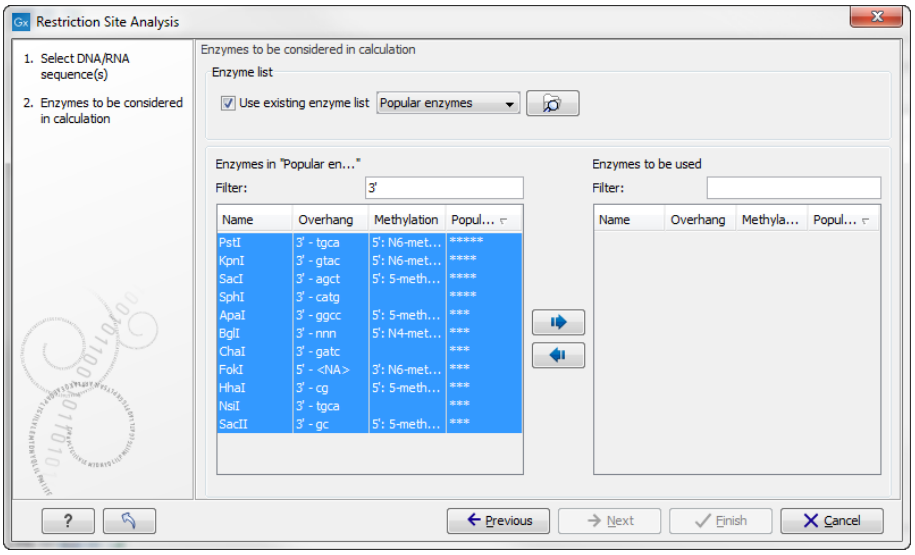

Figure 2.22: *Selecting enzymes.*

View restriction site

The restriction sites are shown in two views: one view is in a tabular format and the other view displays the sites as annotations on the sequence. The result is shown in figure 2.25.

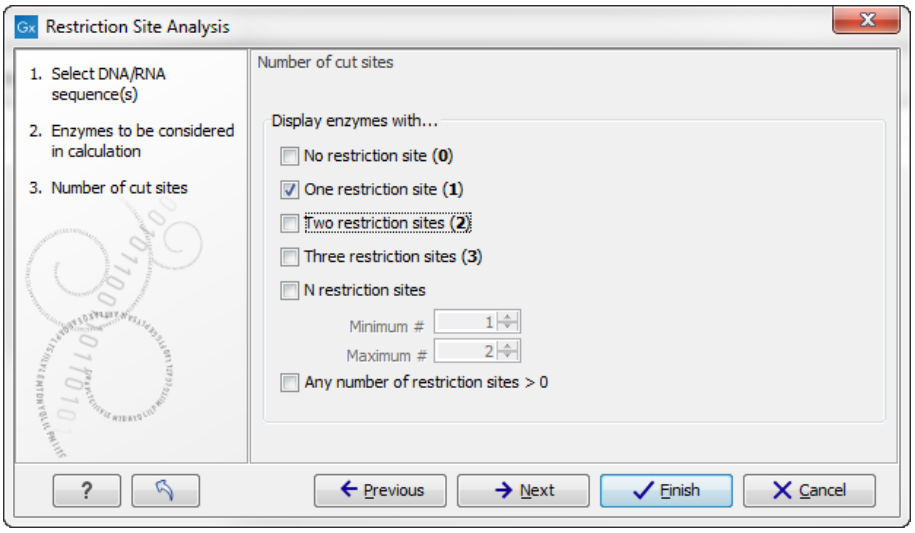

Figure 2.23: *Selecting output for restriction map analysis.*

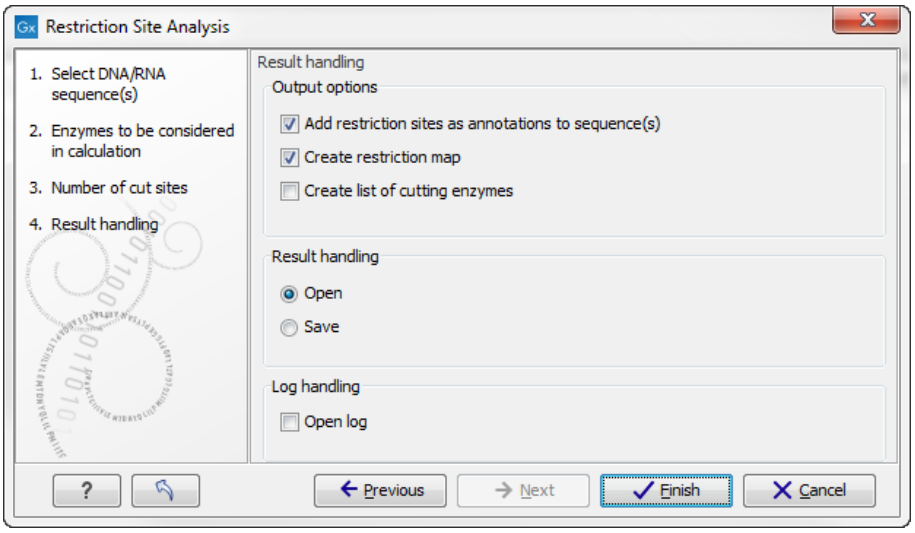

Figure 2.24: *Add restriction sites as annotations on sequence and create restriction map.*

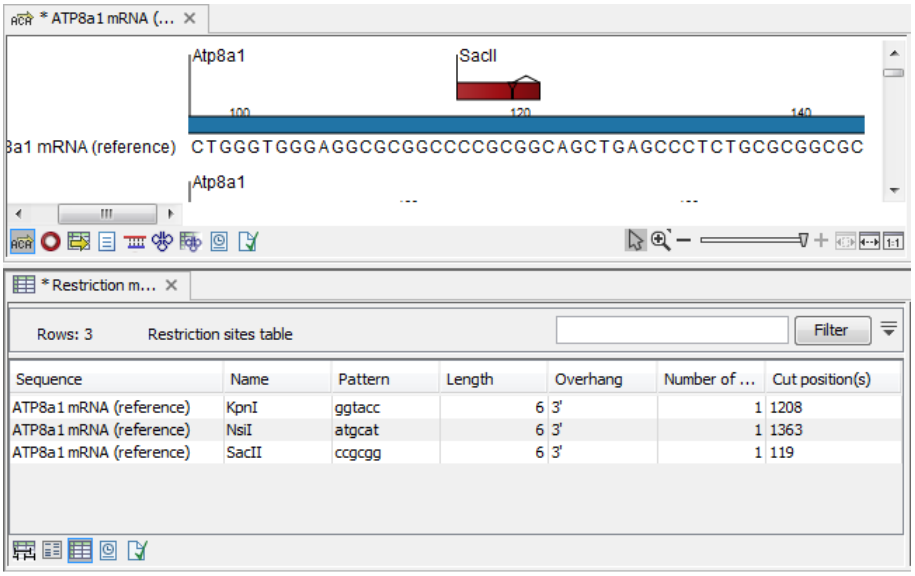

Figure 2.25: *The result of the restriction map analysis is displayed in a table at the bottom and as annotations on the sequence in the view at the top.*

Part II

Core Functionalities

Chapter 3

User interface

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This chapter provides an overview of the different areas in the user interface of *CLC Sequence Viewer*. As can be seen from figure 3.1 this includes a **Navigation Area**, **View Area**, **Menu Bar**, **Toolbar**, **Status Bar** and **Toolbox**.

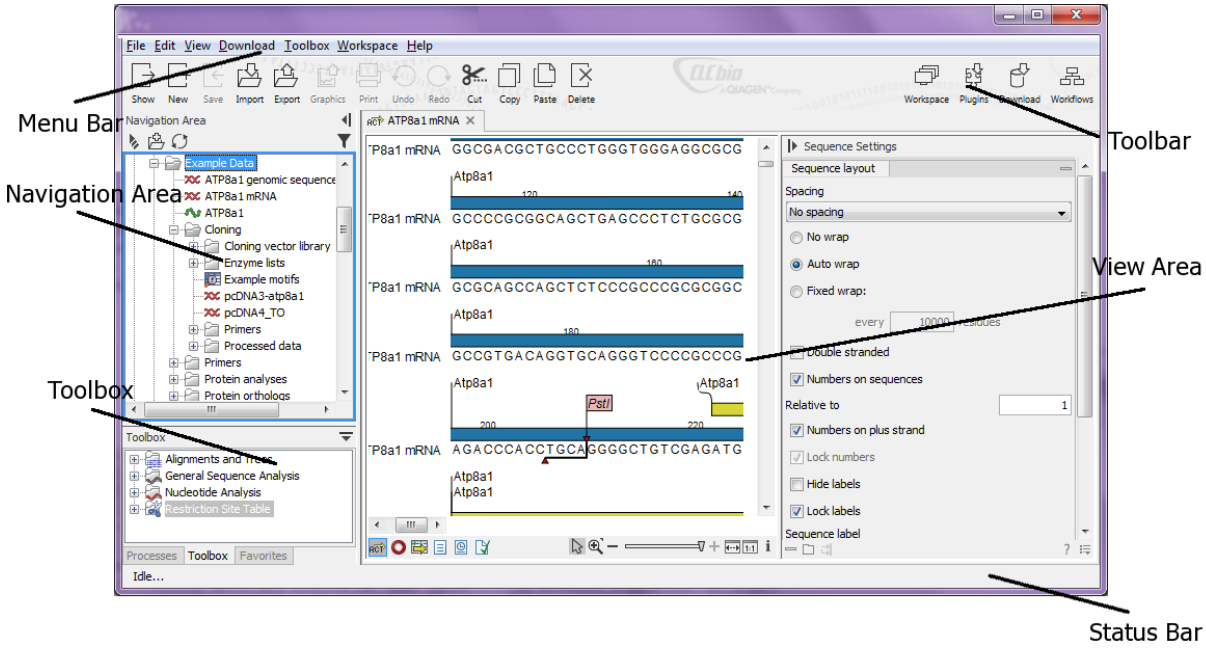

Figure 3.1: *The user interface consists of the Menu Bar, Toolbar, Status Bar, Navigation Area, Toolbox, and View Area.*

3.1 Navigation Area

The **Navigation Area** is located in the left side of the screen, under the **Toolbar** (see figure 3.2). It is used for organizing and navigating data. Its behavior is similar to the way files and folders are usually displayed on your computer.

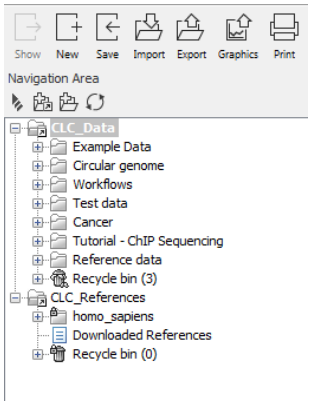

Figure 3.2: *The Navigation Area.*

To provide more space for viewing data, you can hide **Navigation Area** and the **Toolbox** by clicking the hide icon ( ) at the top.

3.1.1 Data structure

The data in the **Navigation Area** is organized into a number of **Locations**. When the *CLC Sequence Viewer* is started for the first time, there is one location called *CLC_Data* (unless your computer administrator has configured the installation otherwise).

A location represents a folder on the computer: The data shown under a location in the **Navigation Area** is stored on the computer in the folder which the location points to.

This is explained visually in figure 3.3. The full path to the system folder can be located by mousing over the data location as shown in figure 3.4.

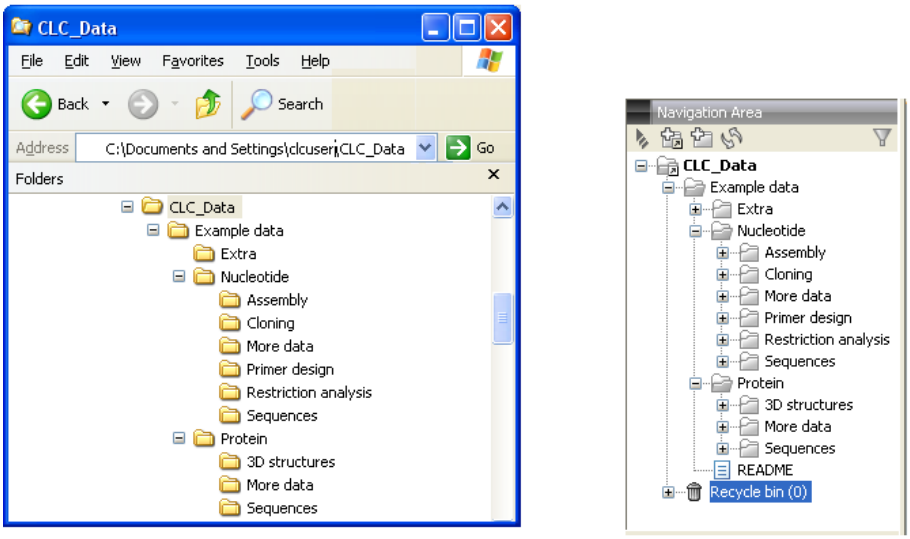

Figure 3.3: *In this example the location called 'CLC_Data' points to the folder at C:\Documents and settings\clcuser\CLC_Data.*

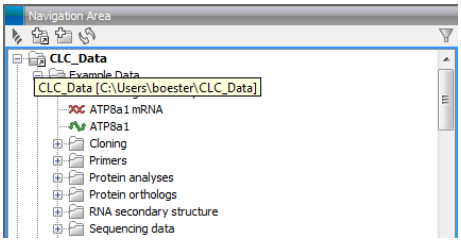

Figure 3.4: *Mousing over the location called 'CLC_Data' shows the full path to the system folder, which in this case is C:\Users\boester\CLC_Data.*

Opening data

The elements in the **Navigation Area** are opened by:

Double-clicking on the element

or **Clicking once on the element** | **Show (→) in the Toolbar**

or **Clicking once on the element** | **Right-click on the element** | **Show (→)**

or **Clicking once on the element** | **Right-click on the element** | **Show (the one without an icon)** | **Select the desired way to view the element from the menu that appears when mousing over "Show"**

This will open a view in the **View Area**, which is described in section 3.2.

Adding data

Data can be added to the **Navigation Area** in a number of ways. Files can be imported from the file system (see chapter 6). Furthermore, an element can be added by dragging it into the **Navigation Area**. This could be views that are open, elements on lists, e.g. search hits or sequence lists, and files located on your computer.

If a file or another element is dropped on a folder, it is placed at the bottom of the folder. If it is dropped on another element, it will be placed just below that element.

If the element already exists in the **Navigation Area** a copy will be created with the name extension "-1", "-2" etc. if more than one copy exist.

3.1.2 Create new folders

In order to organize your files, they can be placed in folders. Creating a new folder can be done in two ways:

right-click an element in the Navigation Area | **New** | **Folder (** **)**

or **File** | **New** | **Folder (** **)**

If a folder is selected in the **Navigation Area** when adding a new folder, the new folder is added at the bottom of this folder. If an element is selected, the new folder is added right above that element.

You can move the folder manually by selecting it and dragging it to the desired destination.

3.1.3 Sorting folders

You can sort the elements in a folder alphabetically:

right-click the folder | **Sort Folder**

On Windows, subfolders will be placed at the top of the folder, and the rest of the elements will be listed below in alphabetical order. On Mac, both subfolders and other elements are listed together in alphabetical order.

3.1.4 Multiselecting elements

Multiselecting elements means that you select more than one element at the same time. This can be done in the following ways:

- Holding down the <Ctrl> key (⌘ on Mac) while clicking on multiple elements selects the elements that have been clicked.
- Selecting one element, and selecting another element while holding down the <Shift> key selects all the elements listed between the two locations (the two end locations included).
- Selecting one element, and moving the curser with the arrow-keys while holding down the <Shift> key, enables you to increase the number of elements selected.

3.1.5 Moving and copying elements

Elements can be moved and copied in several ways:

- Using **Copy** (), **Cut** () and **Paste** () from the **Edit** menu.
- Using Ctrl + C (⌘ + C on Mac), Ctrl + X (⌘ + X on Mac) and Ctrl + V (⌘ + V on Mac).
- Using **Copy** (), **Cut** () and **Paste** () in the **Toolbar**.
- Using drag and drop to move elements.
- Using drag and drop while pressing Ctrl / Command to copy elements.

In the following, all of these possibilities for moving and copying elements are described in further detail.

Copy, cut and paste functions

Copies of elements and folders can be made with the copy/paste function which can be applied in a number of ways:

> **select the files to copy** | **right-click one of the selected files** | **Copy ()** | **right-click the location to insert files into** | **Paste ()**

or **select the files to copy** | **Ctrl + C (⌘ + C on Mac)** | **select where to insert files** | **Ctrl + P (⌘ + P on Mac)**

or **select the files to copy** | **Edit in the Menu Bar** | **Copy ()** | **select where to insert files** | **Edit in the Menu Bar** | **Paste ()**

If there is already an element of that name, the pasted element will be renamed by appending a number at the end of the name.

Elements can also be moved instead of copied. This is done with the cut/paste function:

> **select the files to cut** | **right-click one of the selected files** | **Cut** () | **right-click the location to insert files into** | **Paste ()**

or **select the files to cut** | **Ctrl + X (⌘ + X on Mac)** | **select where to insert files** | **Ctrl + V (⌘ + V on Mac)**

When you have cut the element, it is "grayed out" until you activate the paste function. If you change your mind, you can revert the cut command by copying another element.

Note that if you move data between locations, the original data is kept. This means that you are essentially doing a copy instead of a move operation.

Move using drag and drop

Using drag and drop in the **Navigation Area**, as well as in general, is a four-step process:

> **click the element** | **click on the element again, and hold left mouse button** | **drag the element to the desired location** | **let go of mouse button**

This allows you to:

- Move elements between different folders in the **Navigation Area**
- Drag from the **Navigation Area** to the **View Area**: A new view is opened in an existing **View Area** if the element is dragged from the **Navigation Area** and dropped next to the tab(s) in that **View Area**.
- Drag from the **View Area** to the **Navigation Area**: The element, e.g. a sequence, alignment, search report etc. is saved where it is dropped. If the element already exists, you are asked whether you want to save a copy. You drag from the **View Area** by dragging the tab of the desired element.

Use of drag and drop is supported throughout the program, also to open and re-arrange views (see section 3.2.6).

Note that if you move data between locations, the original data is kept. This means that you are essentially doing a copy instead of a move operation.

Copy using drag and drop

To copy instead of move using drag and drop, hold the Ctrl (⌘ on Mac) key while dragging:

> **click the element | click on the element again, and hold left mouse button | drag the element to the desired location | press Ctrl (⌘ on Mac) while you let go of mouse button release the Ctrl/⌘ button**

3.1.6 Change element names

This section describes two ways of changing the names of sequences in the **Navigation Area**. In the first part, the sequences themselves are not changed - it's their representation that changes. The second part describes how to change the name of the element.

Change how sequences are displayed

Sequence elements can be displayed in the **Navigation Area** with different types of information:

- Name (this is the default information to be shown).
- Accession (sequences downloaded from databases like GenBank have an accession number).
- Latin name.
- Latin name (accession).
- Common name.
- Common name (accession).

Whether sequences can be displayed with this information depends on their origin. Sequences that you have created yourself or imported might not include this information, and you will only be able to see them represented by their name. However, sequences downloaded from databases like GenBank will include this information. To change how sequences are displayed:

right-click any element or folder in the Navigation Area | Sequence Representation | select format

This will only affect sequence elements, and the display of other types of elements, e.g. alignments, trees and external files, will be not be changed. If a sequence does not have this information, there will be no text next to the sequence icon.

Rename element

Renaming a folder or an element in the **Navigation Area** can be done in two different ways:

select the element | Edit in the Menu Bar | Rename

or **select the element | F2**

When you can rename the element, you can see that the text is selected and you can move the cursor back and forth in the text. When the editing of the name has finished; press **Enter** or select another element in the **Navigation Area**. If you want to discard the changes instead, press the **Esc**-key.

3.1.7 Delete, restore and remove elements

When one deletes data from a data folder in the Workbench, it is moved to the recycle bin in that data location. Each data location has its own recycle bin. From the recycle bin, data can then be restored, or completely removed. Removal of data from the recycle bin frees disk space.

Deleting a folder or an element from a Workbench data location can be done in two ways:

right-click the element | Delete ( )

or **select the element | press Delete key**

This will cause the element to be moved to the **Recycle Bin** ( ) where it is kept until the recycle bin is emptied or until you choose to restore the data object to your data location.

For deleting annotations instead of folders or elements, see section 9.3.2.

Items in a recycle bin can be restored in two ways:

Drag the elements with the mouse into the folder where they used to be.

or **select the element | right click and choose the option Restore**.

Once restored, you can continue to work with that data.

All contents of the recycle bin can be removed by choosing to empty the recycle bin:

Edit in the Menu Bar | Empty Recycle Bin ( )

This deletes the data and frees up disk space.

Note! This cannot be undone. Data is not recoverable after it is removed by emptying the recycle bin.

3.1.8 Show folder elements in a table

A location or a folder might contain large amounts of elements. It is possible to view their elements in the **View Area**:

> **select a folder or location** | **Show (→) in the Toolbar**

or

> **select a folder or location** | right click on the folder and select **Show (→)** | **Contents (📁)**

An example is shown in figure 3.5.

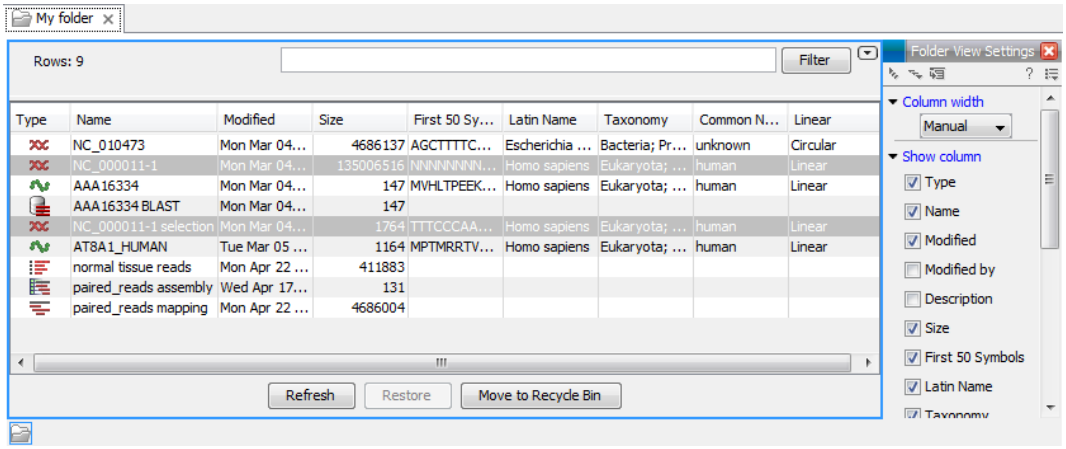

Figure 3.5: *Viewing the elements in a folder.*

When the elements are shown in the view, they can be sorted by clicking the heading of each of the columns. You can further refine the sorting by pressing Ctrl (⌘ on Mac) while clicking the heading of another column.

Sorting the elements in a view does not affect the ordering of the elements in the **Navigation Area**.

Note! The view only displays one "layer" at a time: the content of subfolders is not visible in this view. Also note that only sequences have the full span of information like organism etc.

Batch edit folder elements

You can select a number of elements in the table, right-click and choose **Edit** to batch edit the elements. In this way, you can change for example the description or name of several elements in one go.

In figure 3.6 you can see an example where the name of two sequence are renamed in one go. In this example, a dialog with a text field will be shown, letting you enter a new name for these two sequences.

Note! This information is directly saved and you cannot undo.

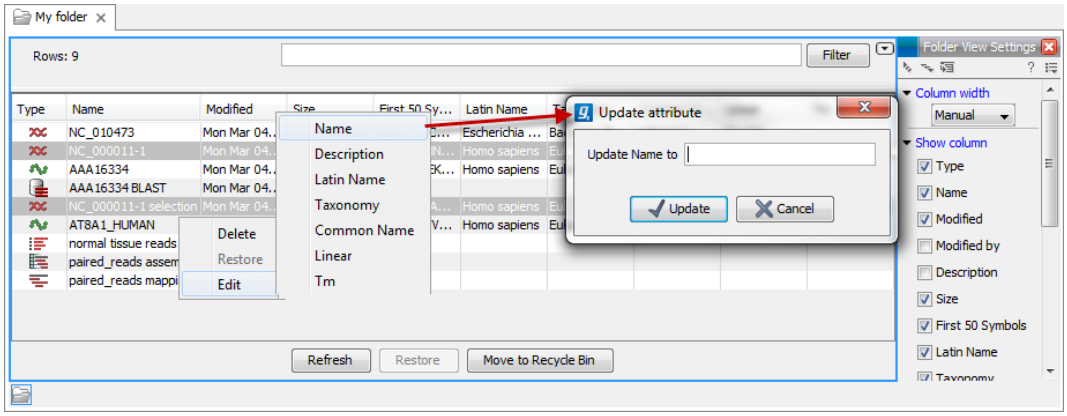

Figure 3.6: *Changing the common name of two sequences.*

Drag and drop folder elements

You can drag and drop objects from the folder editor to the **Navigation area**. This will create a copy of the objects at the selected destination. New elements can be included in the folder editor in the view area by dragging and dropping an element from a destination in the **Navigation Area** to the folder in the **Navigation Area** that you have open in the view area. It is not possible to drag elements directly from the **Navigation Area** to the folder editor in the View area.

3.2 View Area

The **View Area** is the right-hand part of the screen, displaying your current work. The **View Area** may consist of one or more **Views**, represented by tabs at the top of the **View Area**.

This is illustrated in figure 3.7.

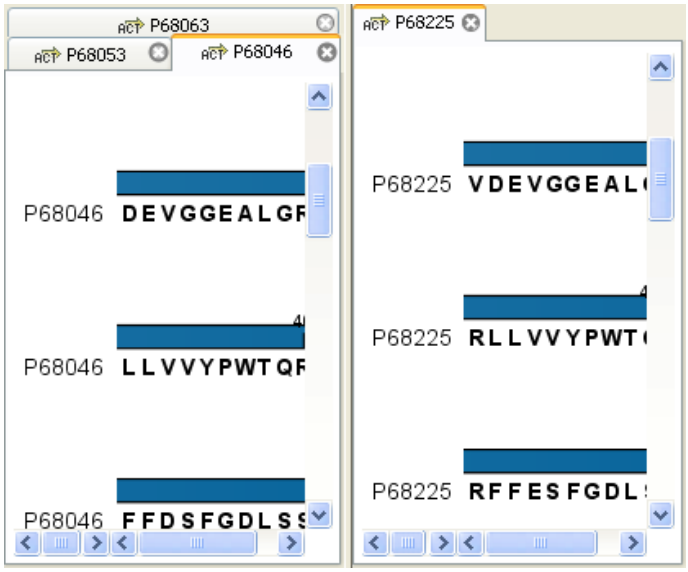

Figure 3.7: *A View Area can enclose several views, each view is indicated with a tab (see right view, which shows protein P68225). Furthermore, several views can be shown at the same time (in this example, four views are displayed).*

The tab concept is central to working with *CLC Sequence Viewer*, because several operations can

be performed by dragging the tab of a view, and extended right-click menus can be activated from the tabs.

This chapter deals with the handling of views inside a **View Area**. Furthermore, it deals with rearranging the views.

Section 3.3 deals with the zooming and selecting functions.

3.2.1 Open view

Opening a view can be done in a number of ways:

double-click an element in the Navigation Area

or **select an element in the Navigation Area | File | Show | Select the desired way to view the element**

or **select an element in the Navigation Area | Ctrl + O (⌘ + B on Mac)**

Opening a view while another view is already open, will show the new view in front of the other view. The view that was already open can be brought to front by clicking its tab.

Note! If you right-click an open tab of any element, click **Show**, and then choose a different view of the same element, this new view is automatically opened in a split-view, allowing you to see both views.

See section 3.1.5 for instructions on how to open a view using drag and drop.

3.2.2 Show element in another view

Each element can be shown in different ways. A sequence, for example, can be shown as linear, circular, text etc.

In the following example, you want to see a sequence in a circular view. If the sequence is already open in a view, you can change the view to a circular view:

Click Show As Circular (⭕) at the lower left part of the view

The buttons used for switching views are shown in figure 3.8).

Figure 3.8: *The buttons shown at the bottom of a view of a nucleotide sequence. You can click the buttons to change the view to e.g. a circular view or a history view.*

If the sequence is already open in a linear view (ACT), and you wish to see both a circular and a linear view, you can split the views very easily:

Press Ctrl (⌘ on Mac) while you | Click Show As Circular (⭕) at the lower left part of the view

This will open a split view with a linear view at the bottom and a circular view at the top (see 9.5).

You can also show a circular view of a sequence without opening the sequence first:

Select the sequence in the Navigation Area | Show ( ) | As Circular ( )

3.2.3 Close views

When a view is closed, the **View Area** remains open as long as there is at least one open view.

A view is closed by:

right-click the tab of the View | Close

or **select the view | Ctrl + W**

or **hold down the Ctrl-button | Click the tab of the view while the button is pressed**

By right-clicking a tab, the following close options exist. See figure 3.9

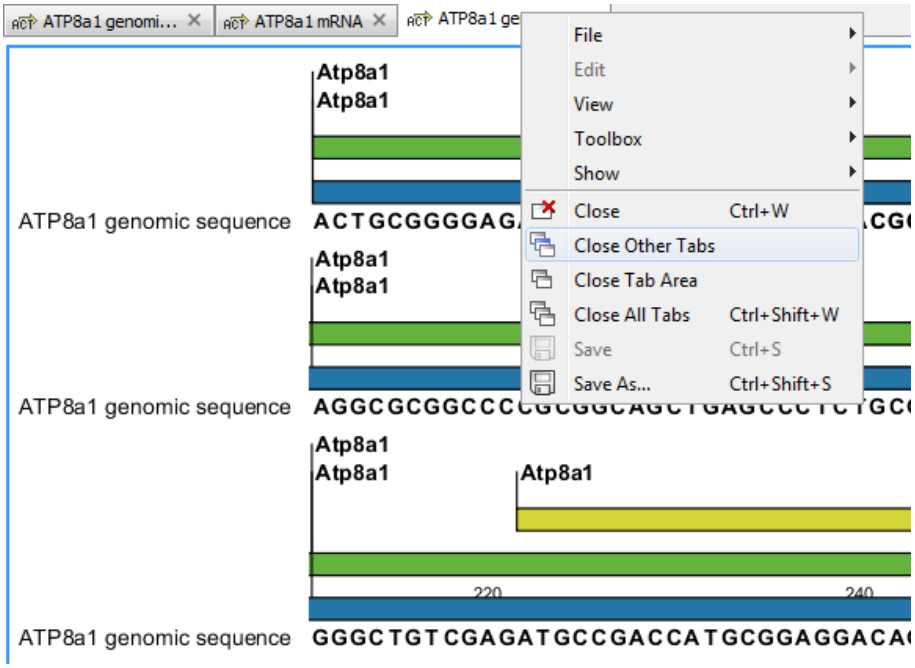

Figure 3.9: *By right-clicking a tab, several close options are available.*

- **Close.** See above.
- **Close Other Tabs.** Closes all other tabs, in all tab areas, except the one that is selected.
- **Close Tab Area.** Closes all tabs in the tab area.
- **Close All Tabs.** Closes all tabs, in all tab areas. Leaves an empty workspace.

3.2.4 Save changes in a view

When changes to an element are made in a view, the text on the tab appears *bold and italic* (on Mac it is indicated by an * before the name of the tab). This indicates that the changes are not saved. The **Save** function may be activated in two ways:

Click the tab of the view you want to save | Save ( ) in the toolbar.

or **Click the tab of the view you want to save | Ctrl + S (⌘ + S on Mac)**

If you close a tab of a view containing an element that has been changed since you opened it, you are asked if you want to save.

When saving an element from a new view that has not been opened from the **Navigation Area** (e.g. when opening a sequence from a list of search hits), a save dialog appears (figure 3.10).

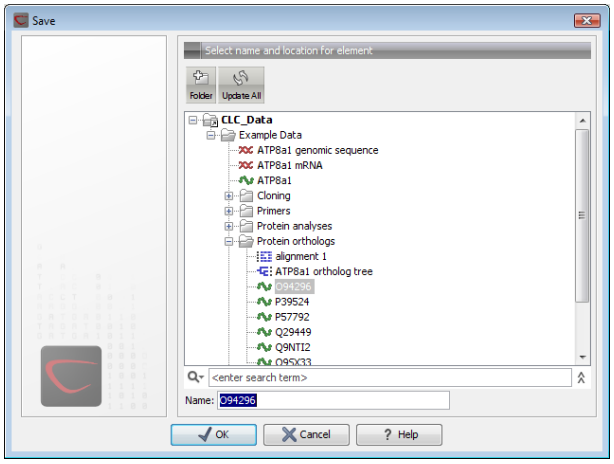

Figure 3.10: *Save dialog.*

In the dialog you select the folder in which you want to save the element.

After naming the element, press **OK**

3.2.5 Undo/Redo

If you make a change to an element in a view, e.g. remove an annotation in a sequence or modify a tree, you can undo the action. In general, **Undo** applies to all changes you can make when right-clicking in a view. **Undo** is done by:

Click undo ( ) in the Toolbar

or **Edit | Undo ( )**

or **Ctrl + Z**

If you want to undo several actions, just repeat the steps above. To reverse the undo action:

Click the redo icon in the Toolbar

or **Edit | Redo ( )**

or **Ctrl + Y**

Note! Actions in the **Navigation Area**, e.g. renaming and moving elements, cannot be undone. However, you can restore deleted elements (see section 3.1.7).

You can set the number of possible undo actions in the Preferences dialog (see section 4).

3.2.6 Arrange views in View Area

To provide more space for viewing data, you can hide **Navigation Area** and the **Toolbox** by clicking the hide icon ( ) at the top of the **Navigation Area**.

Views are arranged in the **View Area** by their tabs. The order of the **views** can be changed using drag and drop. E.g. drag the tab of one view onto the tab of a another. The tab of the first view is now placed at the right side of the other tab.

If a tab is dragged into a view, an area of the view is made gray (see fig. 3.11) illustrating that the view will be placed in this part of the **View Area**.

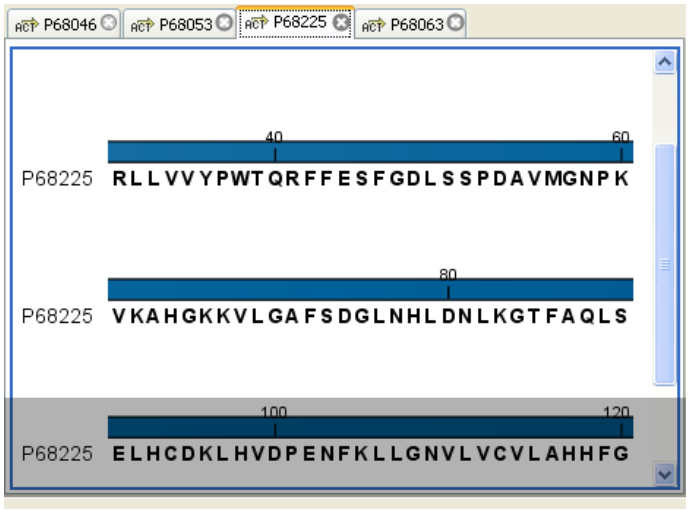

Figure 3.11: *When dragging a view, a gray area indicates where the view will be shown.*

The results of this action is illustrated in figure 3.12.

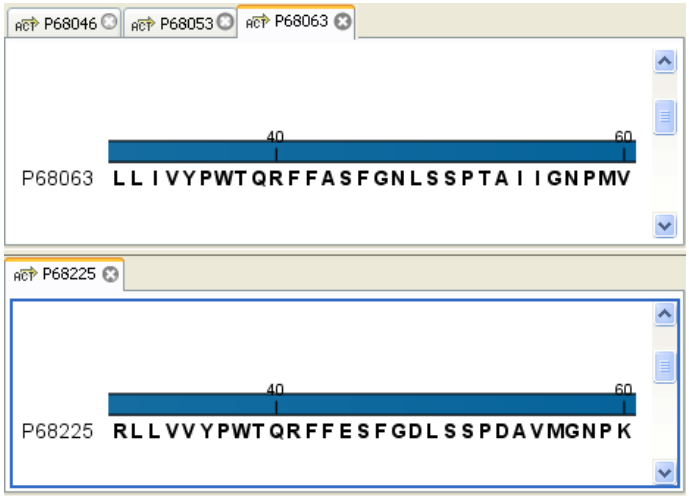

Figure 3.12: *A horizontal split-screen. The two views split the View Area.*

You can also split a **View Area** horizontally or vertically using the menus.

Splitting horizontally may be done this way:

right-click a tab of the view | **View** | **Split Horizontally ( )**

This action opens the chosen view below the existing view. (See figure 3.13). When the split is made vertically, the new view opens to the right of the existing view.

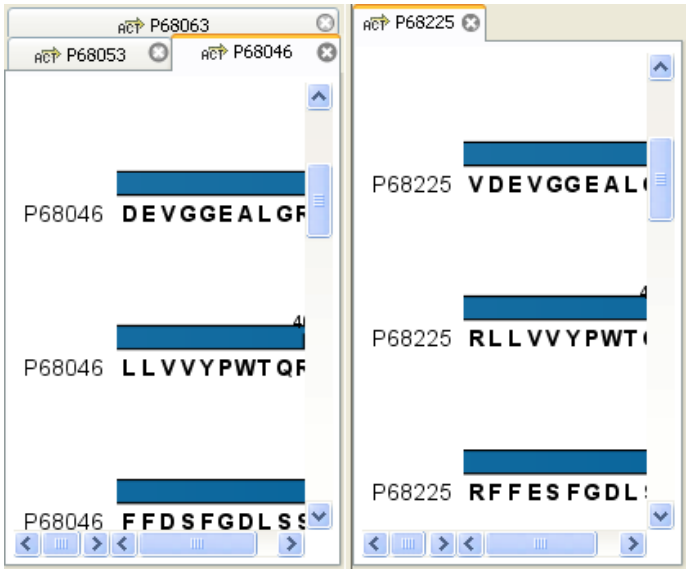

Figure 3.13: *A vertical split-screen.*

Splitting the **View Area** can be undone by dragging e.g. the tab of the bottom view to the tab of the top view. This is marked by a gray area on the top of the view.

Maximize/Restore size of view

The **Maximize/Restore View** function allows you to see a view in maximized mode, meaning a mode where no other **views** nor the **Navigation Area** is shown.

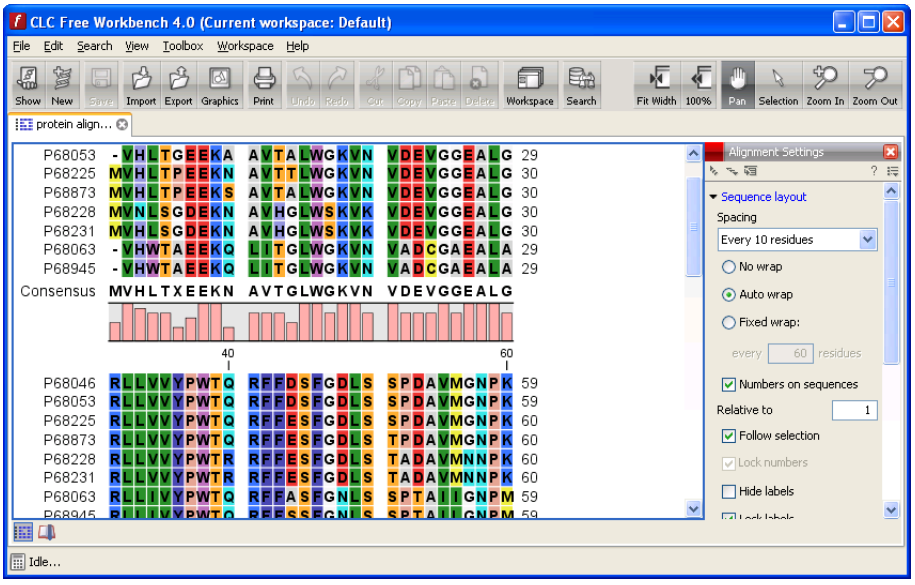

Figure 3.14: *A maximized view. The function hides the Navigation Area and the Toolbox.*

Maximizing a view can be done in the following ways:

select view | **Ctrl + M**

or **select view** | **View** | **Maximize/restore View (**)

or **select view** | **right-click the tab** | **View** | **Maximize/restore View (**)

or **double-click the tab of view**

The following restores the size of the view:

Ctrl + M

or **View** | **Maximize/restore View (**)

or **double-click title of view**

Please note that you can also hide **Navigation Area** and the **Toolbox** by clicking the hide icon ( ) at the top of the **Navigation Area**

3.2.7 Moving a view to a different screen

Using multiple screens can be a great benefit when analyzing data with the *CLC Sequence Viewer*. You can move a view to another screen by dragging the tab of the view and dropping it outside the workbench window. Alternatively, you can right-click in the view area or on the tab itself and select **View | Move to New Window** from the context menu.

An example is shown in figure 3.15, where the main Workbench window shows a table of open reading frames, and the screen to the right is used to display the sequence and annotations.

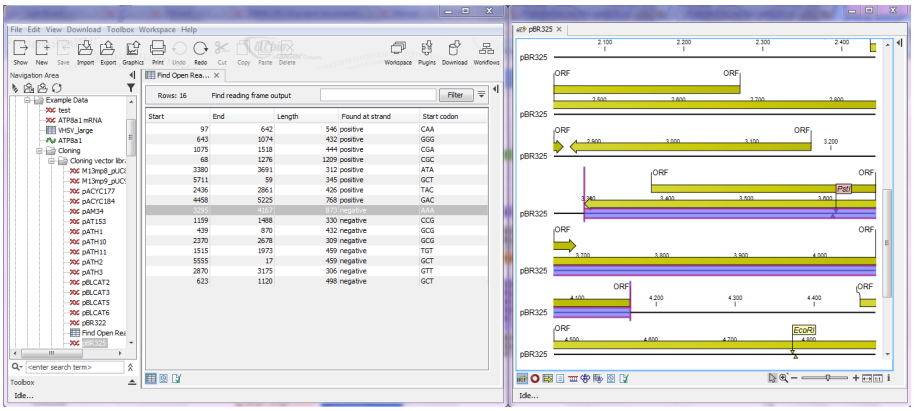

Figure 3.15: *Showing the table on one screen while the sequence is displayed on another screen. Clicking the table of open reading frames causes the view on the other screen to follow the selection. Note that the screen resolution in this figure is kept low in order to include it in the manual; in a real scenario, the resolution will be much higher.*

You can make more detached windows, by dropping tabs outside the open workbench windows, or you can drag more tabs to a detached window. To get a tab back to the main workbench window, just drag the detached tab back, and drop it next to the other tabs in the top of the view area. **Note:** You should not drag the detached window header, just the tab itself.

You can also split the view area in the detached windows as described in section 3.2.6.

3.2.8 Side Panel

The **Side Panel** allows you to change the way the contents of a view are displayed. The options in the **Side Panel** depend on the kind of data in the view, and they are described in the relevant sections about sequences, alignments, trees etc.

Figure 3.16 shows the default **Side Panel** for a protein sequence. It is organized into *palettes*.

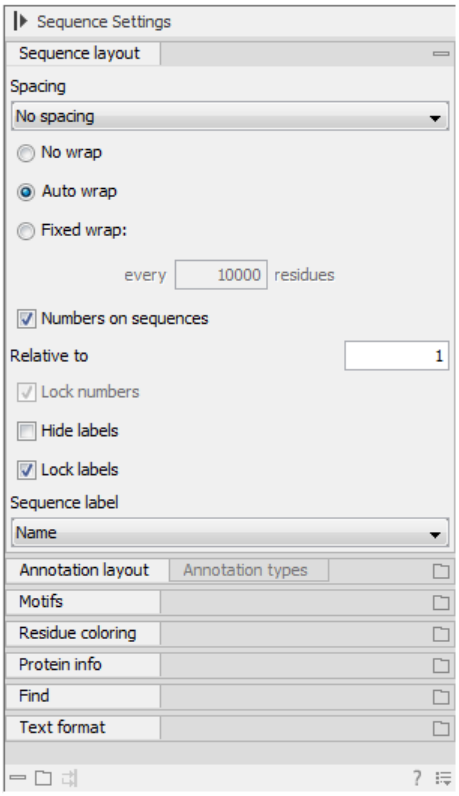

Figure 3.16: *The default view of the Side Panel when opening a protein sequence.*

In this example, there is one for Sequence layout, one for Annotation Layout etc. These palettes can be re-organized by dragging the palette name with the mouse and dropping it where you want it to be. They can either be situated next to each other, so that you can switch between them, or they can be listed on top of each other, so that expanding one of the palettes will push the palettes below further down.

In addition, they can be moved away from the **Side Panel** and placed anywhere on the screen as shown in figure3.17.

In this example, the **Motifs** palette has been placed on top of the sequence view together with the **Protein info** and the **Residue coloring** palettes. In the **Side Panel** to the right, the **Find** palette has been put on top.

In order to make all palettes dock in the **Side Panel** again, click the **Dock Side Panel** icon ( ).

You can completely hide the **Side Panel** by clicking the **Hide Side Panel** icon ( ).

At the bottom of the **Side Panel** (see figure 3.18) there are a number of icons used to:

- Expand all settings ( ).

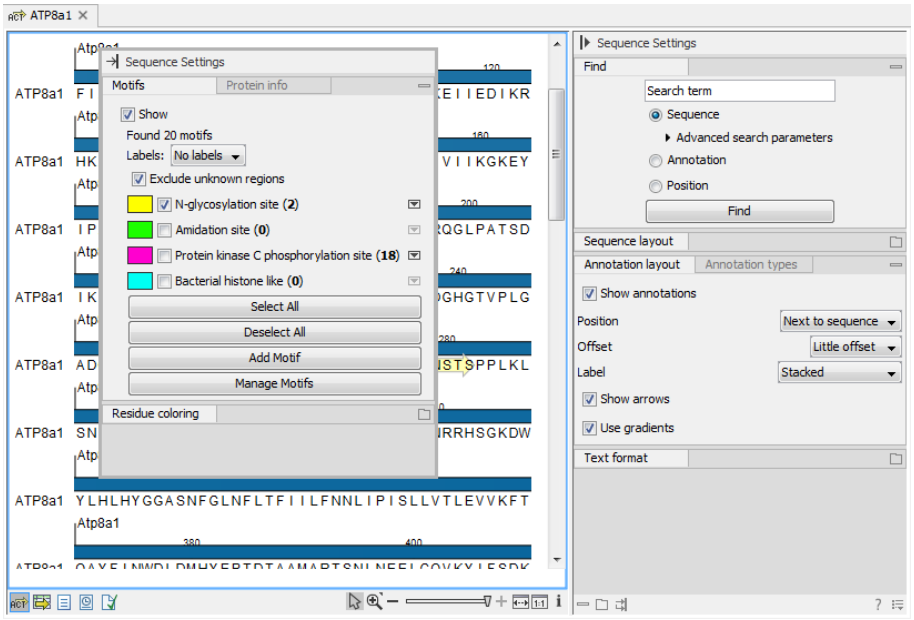

Figure 3.17: *Palettes can be organized in the Side Panel as you like or placed anywhere on the screen.*

- Collapse all settings ( ).
- Dock all palettes ( )
- Get **Help** for the particular view and settings ( )
- Save the settings of the **Side Panel** or apply already saved settings. Read more in section 4.5

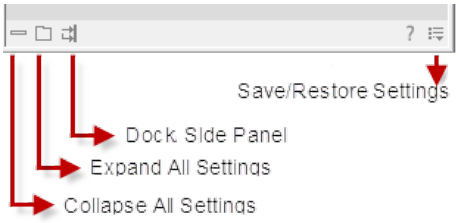

Figure 3.18: *Controlling the Side Panel at the bottom*

Note! Changes made to the **Side Panel**, including the organization of palettes will not be saved when you save the view. See how to save the changes in section 4.5

3.3 Zoom and selection in View Area

All views except tabular and text views support zooming. Figure 3.19 shows the zoom tools, located at the bottom right corner of the view.

The zoom tools consist of some shortcuts for zooming to fit the width of the view ( ), zoom to 100 % to see details ( ), zoom to a selection ( ), a zoom slider, and two mouse mode buttons ( ) ( ).

The slider reflects the current zoom level and can be used to quickly adjust this. For more fine-grained control of the zoom level, move the mouse upwards while sliding.

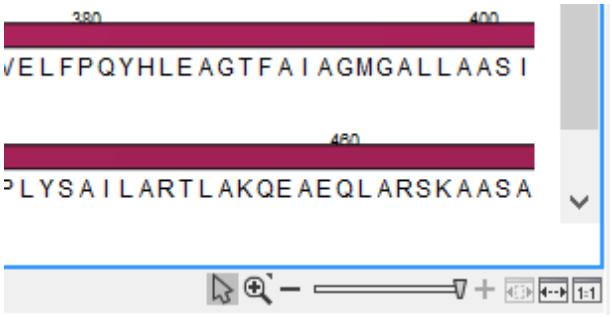

Figure 3.19: *The zoom tools are located at the bottom right corner of the view.*

The sections below describes how to use these tools as well as other ways of zooming and navigating data.

3.3.1 Zoom in

There are six ways of **zooming in**:

Click Zoom in mode (🔍) in the zoom tools (or press Ctrl+2) | click the location in. the view that you want to zoom in on

or **Click Zoom in mode (🔍) in the zoom tools | click-and-drag a box around a part of the view | the view now zooms in on the part you selected**

or **Press '+' on your keyboard**

or **Move the zoom slider located in the zoom tools**

or **Click the plus icon in the zoom tools**

The last option for zooming in is only available if you have a mouse with a scroll wheel:

or **Press and hold Ctrl (⌘ on Mac) | Move the scroll wheel on your mouse forward**

Note! You might have to click in the view before you can use the keyboard or the scroll wheel to zoom.

If you press the **Shift** button on your keyboard while in zoom mode, the zoom function is reversed.

If you want to zoom in to 100 % to see all the data, click the **Zoom to base level** (1:1) icon.

3.3.2 Zoom out

It is possible to zoom out in different ways:

Click Zoom out mode (🔍) in the zoom tools (or press Ctrl+3) | click in the view

or **Press '-' on your keyboard**

or **Move the zoom slider located in the zoom tools**

or **Click the minus icon in the zoom tools**

The last option for zooming out is only available if you have a mouse with a scroll wheel:

or **Press and hold Ctrl (⌘ on Mac) | Move the scroll wheel on your mouse backwards**

Note! You might have to click in the view before you can use the keyboard or the scroll wheel to zoom.

If you want to zoom out to see all the data, click the **Zoom to Fit** ( ) icon.

If you press **Shift** while clicking in a **View**, the zoom function is reversed. Hence, clicking on a sequence in this way while the **Zoom out** mode toolbar item is selected, zooms in instead of zooming out.

3.3.3 Selecting, panning and zooming

In the zoom tools, you can control which mouse mode to use. The default is **Selection mode** ( ) which is used for selecting data in a view. Next to the selection mode, you can select the **Zoom in mode** as described in section 3.3.1. If you press and hold this button, two other modes become available as shown in figure 3.20:

- **Panning** ( ) is used for dragging the view with the mouse as a way of scrolling.
- **Zoom out** ( ) is used to change the mouse mode so that whenever you click the view, it zooms out.

Figure 3.20: *Additional mouse modes can be found in the zoom tools.*

If you hold the mouse over the selection and zoom tools, tooltips will appear that provide further information about how to use the tools.

The mouse modes only apply when the mouse is within the view where they are selected.

The **Selection mode** can also be invoked with the keyboard shortcut Ctrl+1, while the **Panning mode** can be invoked with Ctrl+4.

For some views, if you have made a selection, there is a **Zoom to Selection** ( ) button, which allows you to zoom and scroll directly to fit the view to the selection.

3.4 Toolbox and Status Bar

The **Toolbox** is placed in the left side of the user interface of *CLC Sequence Viewer* below the **Navigation Area**.

The **Toolbox** shows a **Processes tab**, **Favorites tab** and a **Toolbox tab**.

The **Toolbox** can be hidden, so that the **Navigation Area** is enlarged and thereby displays more elements:

View | **Show/Hide Toolbox** | **Show/Hide Toolbox**

You can also click the **Hide Toolbox** ( ) button.

3.4.1 Processes

By clicking the **Processes** tab, the **Toolbox** displays previous and running processes, e.g. an NCBI search or a calculation of an alignment. The running processes can be stopped, paused, and resumed by clicking the small icon ( ) next to the process (see figure 3.21).

Running and paused processes are not deleted.

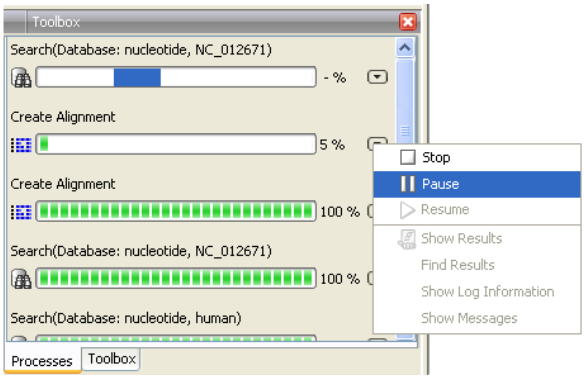

Figure 3.21: *A database search and an alignment calculation are running. Clicking the small icon next to the process allow you to stop, pause and resume processes.*

Besides the options to stop, pause and resume processes, there are some extra options for *a selected number* of the tools running from the Toolbox:

- **Show results**. If you have chosen to save the results (see section 8.1), you will be able to open the results directly from the process by clicking this option.
- **Find results**. If you have chosen to save the results (see section 8.1), you will be able to high-light the results in the Navigation Area.
- **Show Log Information**. This will display a log file showing progress of the process. The log file can also be shown by clicking **Show Log** in the "handle results" dialog where you choose between saving and opening the results.
- **Show Messages**. Some analyses will give you a message when processing your data. The messages are the black dialogs shown in the lower left corner of the Workbench that disappear after a few seconds. You can reiterate the messages that have been shown by clicking this option.

The terminated processes can be removed by:

View | **Remove Finished Processes ( )**

If you close the program while there are running processes, a dialog will ask if you are sure that you want to close the program. Closing the program will stop the process, and it cannot be restarted when you open the program again.

3.4.2 Toolbox

The content of the **Toolbox** tab in the **Toolbox** corresponds to **Toolbox** in the **Menu Bar**.

The tools in the toolbox can be accessed by double-clicking or by dragging elements from the **Navigation Area** to an item in the **Toolbox**.

Quick access to tools

To enable quick launch of tools in *CLC Sequence Viewer*, press Ctrl + Shift + T (⌘ + Shift + T on Mac) to show the quick launch dialog (see figure 3.22).

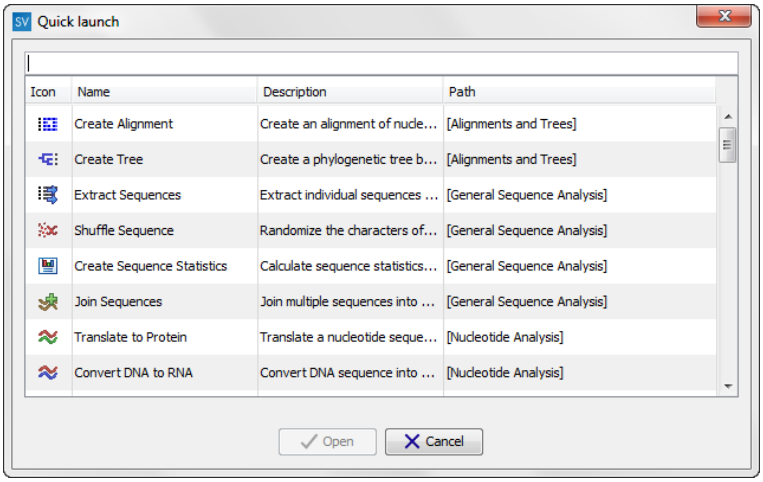

Figure 3.22: *Quick access to all tools in* **CLC Sequence Viewer**.

When the dialog is opened, you can start typing search text in the text field at the top. This will bring up the list of tools that match this text either in the name, description or location in the Toolbox. In the example shown in figure 3.23, typing `create` shows a list of tools involving the word "create", and the arrow keys or mouse can be used for selecting and starting a tool.

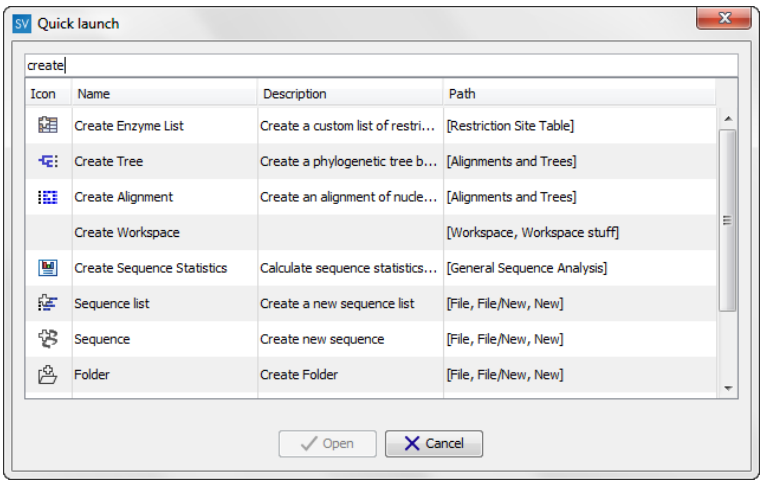

Figure 3.23: *Typing in the search field at the top will filter the list of tools to launch.*

Favorites toolbox

Next to the **Toolbox** tab, you find the **Favorites** tab. This can be used for organizing and getting quick access to the tools you use the most. It consists of two parts as shown in figure 3.24.

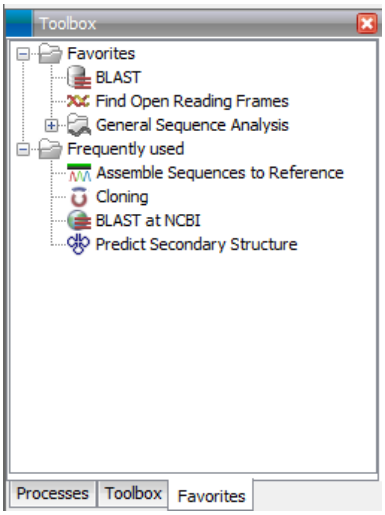

Figure 3.24: *Favorites toolbox.*

Favorites You can manually add tools to the favorites menu simply by right-clicking the tool in the Toolbox. You can also right-click the Favorites folder itself and select **Add Tool**. To remove a tool, right-click and select **Remove from Favorites**. Note that you can also add complete folders to the favorites.

Frequently used The list of tools in this folder is automatically populated as you use the Workbench. The most frequently used tools are listed at the top.

3.4.3 Status Bar

As can be seen from figure 3.1, the **Status Bar** is located at the bottom of the window. In the left side of the bar is an indication of whether the computer is making calculations or whether it is idle. The right side of the **Status Bar** indicates the range of the selection of a sequence. (See chapter 3.3.3 for more about the Selection mode button.)

3.5 Workspace

If you are working on a project and have arranged the views for this project, you can save this arrangement using **Workspaces**. A Workspace remembers the way you have arranged the views, and you can switch between different workspaces.

The **Navigation Area** always contains the same data across **Workspaces**. It is, however, possible to open different folders in the different **Workspaces**. Consequently, the program allows you to display different clusters of the data in separate **Workspaces**.

All **Workspaces** are automatically saved when closing down *CLC Sequence Viewer*. The next time you run the program, the **Workspaces** are reopened exactly as you left them.

Note! It is not possible to run more than one version of *CLC Sequence Viewer* at a time. Use two or more **Workspaces** instead.

3.5.1 Create Workspace

When working with large amounts of data, it might be a good idea to split the work into two or more **Workspaces**. As default the *CLC Sequence Viewer* opens one **Workspace**. Additional **Workspaces** are created in the following way:

Workspace in the Menu Bar) | Create Workspace | enter name of Workspace | OK

When the new **Workspace** is created, the heading of the program frame displays the name of the new **Workspace**. Initially, the selected elements in the **Navigation Area** is collapsed and the **View Area** is empty and ready to work with. (See figure 3.25).

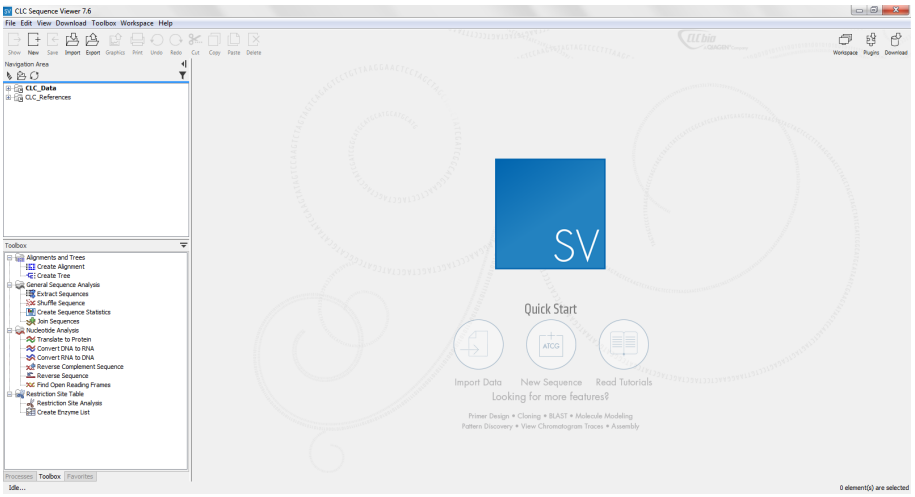

Figure 3.25: *An empty Workspace.*

3.5.2 Select Workspace

When there is more than one **Workspace** in the *CLC Sequence Viewer*, there are two ways to switch between them:

Workspace ( ) in the Toolbar | Select the Workspace to activate

or **Workspace in the Menu Bar | Select Workspace ( ) | choose which Workspace to activate | OK**

The name of the selected **Workspace** is shown after "*CLC Sequence Viewer*" at the top left corner of the main window, in figure 3.25 it says: (default).

3.5.3 Delete Workspace

Deleting a **Workspace** can be done in the following way:

Workspace in the Menu Bar | Delete Workspace | choose which Workspace to delete | OK

Note! Be careful to select the right **Workspace** when deleting. The delete action cannot be undone. (However, no data is lost, because a workspace is only a representation of data.)

It is not possible to delete the default workspace.

3.6 List of shortcuts

The keyboard shortcuts in *CLC Sequence Viewer* are listed below.

Action	Windows/Linux	Mac OS X
Adjust selection	Shift + arrow keys	Shift + arrow keys
Adjust workflow layout	Shift + Alt + L	⌘ + Shift + Alt + L
BLAST	Ctrl + Shift + L	⌘ + Shift + L
BLAST at NCBI	Ctrl + Shift + B	⌘ + Shift + B
Close	Ctrl + W	⌘ + W
Close all views	Ctrl + Shift + W	⌘ + Shift + W
Copy	Ctrl + C	⌘ + C
Create alignment	Ctrl + Shift + A	⌘ + Shift + A
Create track list	Ctrl + L	⌘ + L
Cut	Ctrl + X	⌘ + X
Delete	Delete	Delete or ⌘ + Backspace
Exit	Alt + F4	⌘ + Q
Export	Ctrl + E	⌘ + E
Export graphics	Ctrl + G	⌘ + G
Find Next Conflict	'.' (dot)	'.' (dot)
Find Previous Conflict	',' (comma)	',' (comma)
Help	F1	F1
Import	Ctrl + I	⌘ + I
Maximize/restore size of View	Ctrl + M	⌘ + M
Move gaps in alignment	Ctrl + arrow keys	⌘ + arrow keys
New Folder	Ctrl + Shift + N	⌘ + Shift + N
New Sequence	Ctrl + N	⌘ + N
Panning Mode	Ctrl + 4	⌘ + 4
Paste	Ctrl + V	⌘ + V
Print	Ctrl + P	⌘ + P
Redo	Ctrl + Y	⌘ + Y
Rename	F2	F2
Reverse zoom mode	press and hold Shift	press and hold Shift
Save	Ctrl + S	⌘ + S
Save As	Ctrl + Shift + S	⌘ + Shift + S
Scrolling horizontally	Shift + Scroll wheel	Shift + Scroll wheel
Search local data	Ctrl + Shift + F	⌘ + Shift + F
Search via Side Panel	Ctrl + F	⌘ + F
Search NCBI	Ctrl + B	⌘ + B
Search UniProt	Ctrl + Shift + U	⌘ + Shift + U
Select All	Ctrl + A	⌘ + A
Select Selection Mode	Ctrl + 1 (one)	⌘ + 1 (one)
Show folder content	Ctrl + O	⌘ + O
Show/hide Side Panel	Ctrl + U	⌘ + U
Sort folder	Ctrl + Shift + R	⌘ + Shift + R
Split Horizontally	Ctrl + T	⌘ + T
Split Vertically	Ctrl + J	⌘ + J
Start Tool Quick Launch	Ctrl + Shift + T	⌘ + Shift + T
Translate to Protein	Ctrl + Shift + P	⌘ + Shift + P
Undo	Ctrl + Z	⌘ + Z
Update folder	F5	F5
User Preferences	Ctrl + K	⌘ + ;

Action	Windows/Linux	Mac OS X
Vertical scroll in read tracks	Alt + Scroll wheel	Alt + Scroll wheel
Vertical scroll in reads tracks, fast	Shift+Alt+Scroll wheel	Shift+Alt+Scroll wheel
Vertical zoom in graph tracks	Alt + Scroll wheel	Alt + Scroll wheel
Workflow, add element	Alt + Shift + E	Alt + Shift + E
Workflow, collapse if its expanded	Alt + Shift + '-' (minus)	Alt + Shift + '-'
Workflow, create installer	Alt + Shift + I	Alt + Shift + I
Workflow, execute	Ctrl + enter	⌘ + enter
Workflow, expand if its collapsed	Alt + Shift + '+' (plus)	Alt + Shift + '-'
Workflow, highlight used elements	Alt + Shift + U	Alt + Shift + U
Workflow, remove all elements	Alt + Shift + R	Alt + Shift + R
Zoom	Ctrl + Scroll wheel	Ctrl + Scroll wheel
Zoom In Mode	Ctrl + 2	⌘ + 2
Zoom In (without clicking)	'+' (plus)	'+' (plus)
Zoom Out Mode	Ctrl + 3	⌘ + 3
Zoom Out (without clicking)	'-' (minus)	'-' (minus)
Zoom to base level	Ctrl + 0	⌘ + 0
Zoom to fit screen	Ctrl + 6	⌘ + 6
Zoom to selection	Ctrl + 5	⌘ + 5

Combinations of keys and mouse movements are listed below.

Action	Windows/Linux	Mac OS X	Mouse movement
Maximize View			Double-click the tab of the View
Restore View			Double-click the View title
Reverse zoom mode	Shift	Shift	Click in view
Select multiple elements that are not grouped together	Ctrl	⌘	Click elements
Select multiple elements that are grouped together	Shift	Shift	Click elements

"Elements" in this context refers to elements and folders in the **Navigation Area** selections on sequences, and rows in tables.

Chapter 4

User preferences and settings

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4.5.1 Saving, removing and applying saved settings 70

The first three sections in this chapter deal with the general preferences that can be set for *CLC Sequence Viewer* using the **Preferences** dialog. The next section explains how the settings in the **Side Panel** can be saved and applied to other views. Finally, you can learn how to import and export the preferences.

The **Preferences** dialog offers opportunities for changing the default settings for different features of the program.

The **Preferences** dialog is opened in one of the following ways and can be seen in figure 4.2:

Edit | Preferences ( )

or **Ctrl + K (⌘ + ; on Mac)**

4.1 General preferences

The **General** preferences include:

- **Undo Limit.** As default the undo limit is set to 500. By writing a higher number in this field, more actions can be undone. Undo applies to all changes made on molecules, sequences, alignments or trees. See section 3.2.5 for more on this topic.

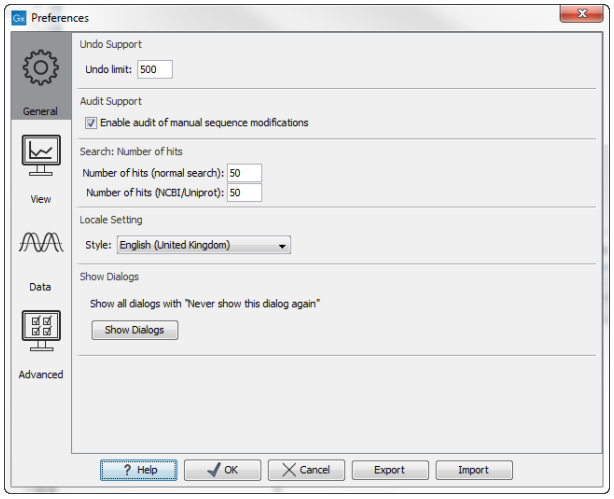

Figure 4.1: *Preferences include General preferences, View preferences, Data preferences, and Advanced settings.*

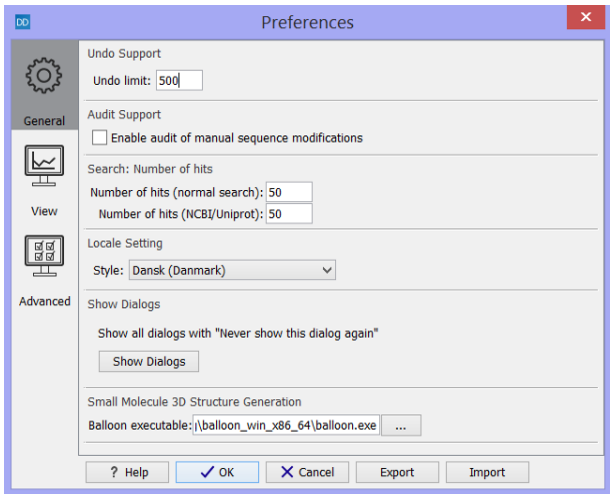

Figure 4.2: *Preferences include General preferences, View preferences, Data preferences, and Advanced settings.*

- **Audit Support.** If this option is checked, all manual editing of sequences will be marked with an annotation on the sequence (see figure 4.3). Placing the mouse on the annotation will reveal additional details about the change made to the sequence (see figure 4.4). Note that no matter whether **Audit Support** is checked or not, all changes are also recorded in the **History** ( ) (see section 7).
- **Number of hits.** The number of hits shown in *CLC Sequence Viewer*, when e.g. searching NCBI. (The sequences shown in the program are not downloaded, until they are opened or dragged/saved into the Navigation Area).
- **Locale Setting.** Specify which country you are located in. This determines how punctation is used in numbers all over the program.
- **Show Dialogs.** A lot of information dialogs have a checkbox: "Never show this dialog again". When you see a dialog and check this box in the dialog, the dialog will not be shown again. If you regret and wish to have the dialog displayed again, click the button in the General Preferences: **Show Dialogs**. Then all the dialogs will be shown again.

Figure 4.3: *Annotations added when the sequence is edited.*

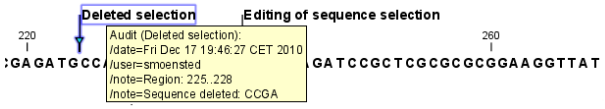

Figure 4.4: *Details of the editing.*

4.2 Default view preferences

There are six groups of default **View** settings:

1. **Toolbar**
2. **Show Side Panel**
3. **New View**
4. **Sequence Representation**
5. **User Defined View Settings**
6. **Molecule Project 3D Editor**

In general, these are default settings for the user interface.

The **Toolbar preferences** let you choose the size of the toolbar icons, and you can choose whether to display names below the icons.

The **Show Side Panel** setting allows you to choose whether to display the side panel.

The **New view** setting allows you to choose whether the **View preferences** are to be shown automatically when opening a new view. If this option is not chosen, you can press (Ctrl + U (⌘ + U on Mac)) to see the preferences panels of an open view.

The **Sequence Representation** allows you to change the way the elements appear in the **Navigation Area**. The following text can be used to describe the element:

- Name (this is the default information to be shown).
- Accession (sequences downloaded from databases like GenBank have an accession number).
- Latin name.
- Latin name (accession).
- Common name.
- Common name (accession).

The **User Defined View Settings** gives you an overview of the different **Side Panel** settings that are saved for each view. See section 4.5 for more about how to create and save style sheets.

If there are other settings beside **CLC Standard Settings**, you can use this overview to choose which of the settings should be used per default when you open a view (see an example in figure 4.5).

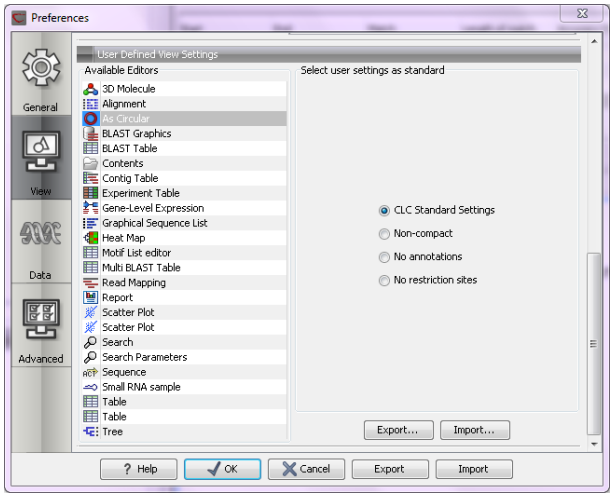

Figure 4.5: *Selecting the default view setting.*

In this example, the **CLC Standard Settings** is chosen as default.

The **Molecule Project 3D Editor** gives you the option to turn off the modern OpenGL rendering for **Molecule Projects** (see section 10.2.2).

4.2.1 Number formatting in tables

In the preferences, you can specify how the numbers should be formatted in tables (see figure 4.6).

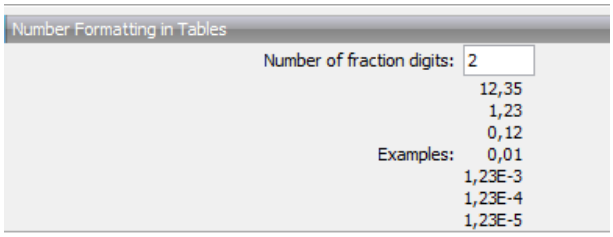

Figure 4.6: *Number formatting of tables.*

The examples below the text field are updated when you change the value so that you can see the effect. After you have changed the preference, you have to re-open your tables to see the effect.

4.2.2 Import and export Side Panel settings

If you have created a special set of settings in the **Side Panel** that you wish to share with other CLC users, you can export the settings in a file. The other user can then import the settings.

To export the **Side Panel** settings, first select the views that you wish to export settings for. Use Ctrl+click (⌘ + click on Mac) or Shift+click to select multiple views. Next click the **Export...**button. Note that there is also another export button at the very bottom of the dialog, but this will export the other settings of the **Preferences** dialog (see section 4.4).

A dialog will be shown (see figure 4.7) that allows you to select which of the settings you wish to export.

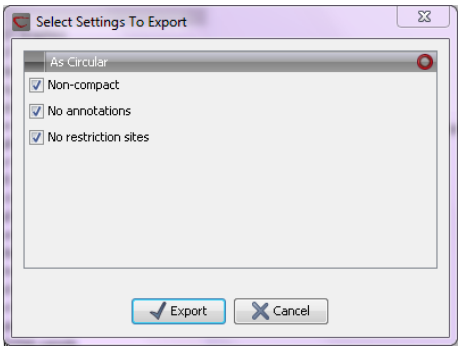

Figure 4.7: *Exporting all settings for circular views.*

When multiple views are selected for export, all the view settings for the views will be shown in the dialog. Click **Export** and you will now be able to define a save folder and name for the exported file. The settings are saved in a file with a .vsf extension (View Settings File).

To import a **Side Panel** settings file, make sure you are at the bottom of the **View** panel of the **Preferences dialog**, and click the **Import...** button. Note that there is also another import button at the very bottom of the dialog, but this will import the other settings of the **Preferences** dialog (see section 4.4).

The dialog asks if you wish to overwrite existing **Side Panel** settings, or if you wish to merge the imported settings into the existing ones (see figure 4.8).

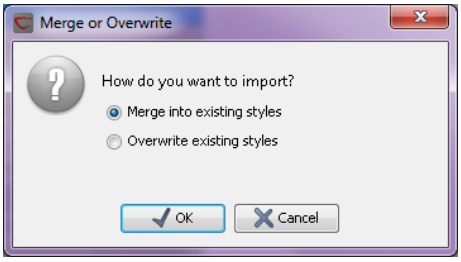

Figure 4.8: *When you import settings, you are asked if you wish to overwrite existing settings or if you wish to merge the new settings into the old ones.*

Note! If you choose to overwrite the existing settings, you will loose all the **Side Panel** settings that you have previously saved.

To avoid confusion of the different import and export options, here is an overview:

- Import and export of **bioinformatics data** such as sequences, alignments etc. (described in section 6.1).
- **Graphics** export of the views which creates image files in various formats (described in section 6.3).

- Import and export of **Side Panel Settings** as described above.
- Import and export of all the **Preferences** except the Side Panel settings. This is described in the previous section.

4.3 Advanced preferences

The **Advanced** settings include the possibility to set up a proxy server. This is described in section 1.7.

4.4 Export/import of preferences

The user preferences of the *CLC Sequence Viewer* can be exported to other users of the program, allowing other users to display data with the same preferences as yours. You can also use the export/import preferences function to backup your preferences.

To export preferences, open the **Preferences** dialog (Ctrl + K (⌘ + ; on Mac)) and do the following:

> **Export** | **Select the relevant preferences** | **Export** | **Choose location for the exported file** | **Enter name of file** | **Save**

Note! The format of exported preferences is .cpf. This notation must be submitted to the name of the exported file in order for the exported file to work.

Before exporting, you are asked about which of the different settings you want to include in the exported file. One of the items in the list is "User Defined View Settings". If you export this, only the information about which of the settings is the default setting for each view is exported. If you wish to export the **Side Panel Settings** themselves, see section 4.2.2.

The process of importing preferences is similar to exporting:

> **Press Ctrl + K (⌘ + ; on Mac) to open Preferences** | **Import** | **Browse to and select the .cpf file** | **Import and apply preferences**

4.4.1 The different options for export and import

To avoid confusion of the different import and export options, you can find an overview here:

- Import and export of **bioinformatics data** such as molecules, sequences, alignments etc. (described in section 6.1).
- **Graphics** export of the views that create image files in various formats (described in section 6.3).
- Import and export of **Side Panel Settings** as described in the next section.
- Import and export of all the **Preferences** except the Side Panel settings. This is described above.

4.5 View settings for the Side Panel

The **Side Panel** is shown to the right of all views that are opened in *CLC Sequence Viewer* and is described in further detail in section 3.2.8.

When you have adjusted a view of e.g. a sequence, your settings in the **Side Panel** can be saved. When you open other sequences, which you want to display in a similar way, the saved settings can be applied. The options for saving and applying are available at the bottom of the **Side Panel** (see figure 4.9).

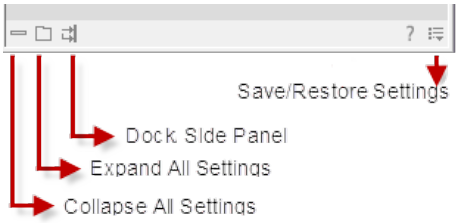

Figure 4.9: *At the bottom of the Side Panel you save the view settings*

4.5.1 Saving, removing and applying saved settings

To save and apply the saved settings, click ( ) seen in figure 4.9. This opens a menu where the following options are available (figure 4.10):

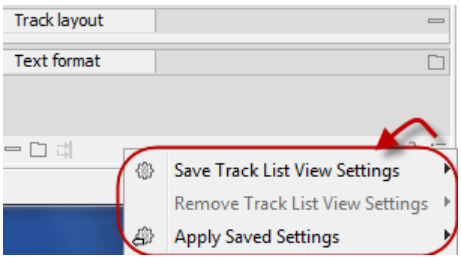

Figure 4.10: *When you have adjusted the side panel settings and would like to save these, this can be done with the "Save ... Settings" function, where "..." is the element you are working on - e.g. "Track List View", "Sequence View", "Table View", "Alignment View" etc. Saved settings can be deleted again with "Remove ... Settings" and can be applied to other elements with "Apply Saved Settings".*

- **Save ... Settings.** ( ) The settings can be saved in two different ways. When you select either way of saving settings a dialog will open (see figure 4.11) where you can enter a name for your settings.
  - **For ... View in General** ( ) Will save the currently used settings with all elements of the same type as the one used for adjusting the settings. E.g. if you have selected to save settings "For Track View in General" the settings will be applied each time you open an element of the same type, which in this case means each time one of the saved tracks are opened from the **Navigation Area**. These "general" settings are user specific and will not be saved with or exported with the element.
  - **On This Only** ( ) Settings can be saved with the specific element that you are working on in the View area and will not affect any other elements (neither in the View Area or

in the **Navigation Area**). E.g. for a track you would get the option to save settings "On This Track Only". The settings are saved with only this element (and will be exported with the element if you later select to export the element to another destination).

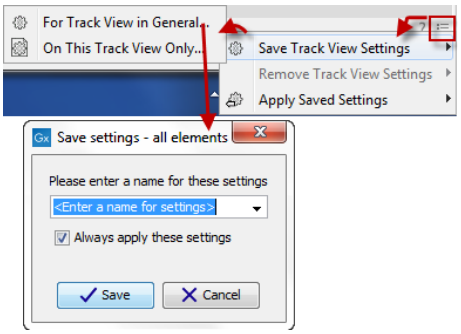

Figure 4.11: *The save settings dialog.Two options exist for saving settings. Click on the relevant option to open the dialog shown at the bottom of the figure.*

- **Remove ... Settings.** ( ) Gives you the option to remove settings specifically for the element that you are working on in the View Area, or on all elements of the same type. When you have selected the relevant option, the dialog shown in figure 4.12 opens and allows you to select which of the saved settings to remove.
  - **From ... View in General** ( ) Will remove the currently used settings on all elements of the same type as the one used for adjusting the settings. E.g. if you have selected to remove settings from all alignments using "From Alignment View in General", all alignments in your **Navigation Area** will be opened with the standard settings in stead.
  - **From This ... Only** ( ) When you select this option, the selected settings will only be removed from the particular element that you are working on in the View area and will not affect any other elements (neither in the View Area or in the **Navigation Area**). The settings for this particular element will be replaced with the CLC standard settings ( ).

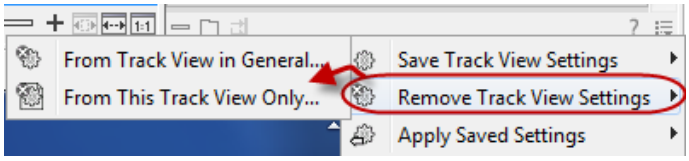
From Track View in General...
From This Track View Only...
Save Track View Settings
Remove Track View Settings
Apply Saved Settings

Figure 4.12: *The remove settings dialog for a track.*

- **Apply Saved Settings.** ( ) This is a submenu containing the settings that you have previously saved (figure 4.13). By clicking one of the settings, they will be applied to the current view. You will also see a number of pre-defined view settings in this submenu. They are meant to be examples of how to use the **Side Panel** and provide quick ways of adjusting the view to common usages. At the bottom of the list of settings you will see **CLC Standard Settings** which represent the way the program was set up, when you first launched it. ( )

The settings are specific to the type of view. Hence, when you save settings of a circular view, they will not be available if you open the sequence in a linear view.

If you wish to export the settings that you have saved, this can be done in the **Preferences** dialog under the **View** tab (see section 4.2.2).

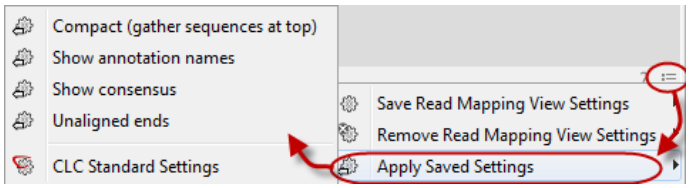

Figure 4.13: *Applying saved settings.*

Chapter 5

Printing

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CLC Sequence Viewer offers different choices of printing the result of your work.

This chapter deals with printing directly from *CLC Sequence Viewer*. Another option for using the graphical output of your work, is to export graphics (see chapter 6.3) in a graphic format, and then import it into a document or a presentation.

All the kinds of data that you can view in the **View Area** can be printed. The *CLC Sequence Viewer* uses a WYSIWYG principle: What You See Is What You Get. This means that you should use the options in the Side Panel to change how your data, e.g. a sequence, looks on the screen. When you print it, it will look exactly the same way on print as on the screen.

For some of the views, the layout will be slightly changed in order to be printer-friendly.

It is not possible to print elements directly from the **Navigation Area**. They must first be opened in a view in order to be printed. To print the contents of a view:

select relevant view | Print (🖶) in the toolbar

This will show a print dialog (see figure 5.1).

In this dialog, you can:

- Select which part of the view you want to print.
- Adjust **Page Setup**.
- See a print **Preview** window.

These three options are described in the three following sections.

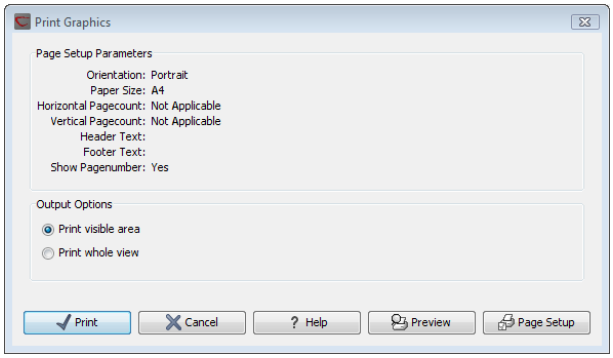

Figure 5.1: *The Print dialog.*

5.1 Selecting which part of the view to print

In the print dialog you can choose to:

- **Print visible area**, or
- **Print whole view**

These options are available for all views that can be zoomed in and out. In figure 5.2 is a view of a circular sequence which is zoomed in so that you can only see a part of it.

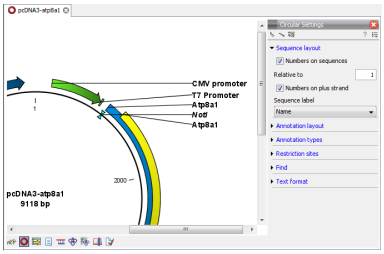

Figure 5.2: *A circular sequence as it looks on the screen.*

When selecting **Print visible area**, your print will reflect the part of the sequence that is *visible* in the view. The result from printing the view from figure 5.2 and choosing **Print visible area** can be seen in figure 5.3.

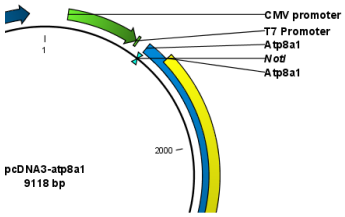

Figure 5.3: *A print of the sequence selecting Print visible area.*

On the other hand, if you select **Print whole view**, you will get a result that looks like figure 5.4. This means that you also print the part of the sequence which is not visible when you have zoomed in.

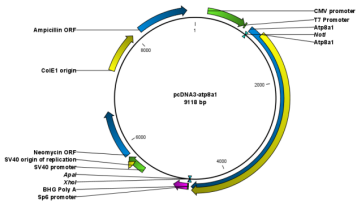

Figure 5.4: *A print of the sequence selecting Print whole view. The whole sequence is shown, even though the view is zoomed in on a part of the sequence.*

5.2 Page setup

No matter whether you have chosen to print the visible area or the whole view, you can adjust page setup of the print. An example of this can be seen in figure 5.5

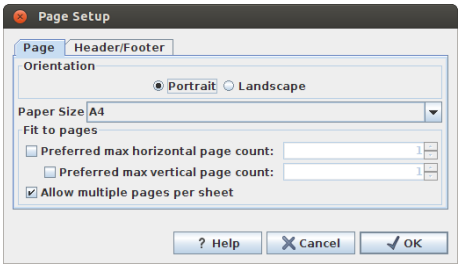

Figure 5.5: *Page Setup.*

In this dialog you can adjust both the setup of the pages and specify a header and a footer by clicking the tab at the top of the dialog.

You can modify the layout of the page using the following options:

- **Orientation**.
  - **Portrait**. Will print with the paper oriented vertically.
  - **Landscape**. Will print with the paper oriented horizontally.
- **Paper size**. Adjust the size to match the paper in your printer.
- **Fit to pages**. Can be used to control how the graphics should be split across pages (see figure 5.6 for an example).
  - **Horizontal pages**. If you set the value to e.g. 2, the printed content will be broken up horizontally and split across 2 pages. This is useful for sequences that are not wrapped
  - **Vertical pages**. If you set the value to e.g. 2, the printed content will be broken up vertically and split across 2 pages.

Note! It is a good idea to consider adjusting view settings (e.g. **Wrap** for sequences), in the **Side Panel** before printing. As explained in the beginning of this chapter, the printed material will look like the view on the screen, and therefore these settings should also be considered when adjusting **Page Setup**.

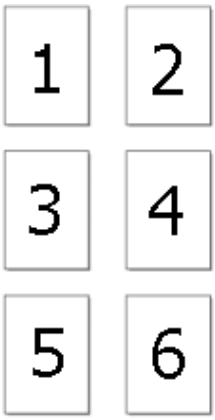

Figure 5.6: *An example where Fit to pages horizontally is set to 2, and Fit to pages vertically is set to 3.*

5.2.1 Header and footer

Click the **Header/Footer** tab to edit the header and footer text. By clicking in the text field for either **Custom header text** or **Custom footer text** you can access the auto formats for header/footer text in **Insert a caret position**. Click either **Date**, **View name**, or **User name** to include the auto format in the header/footer text.

Click **OK** when you have adjusted the **Page Setup**. The settings are saved so that you do not have to adjust them again next time you print. You can also change the **Page Setup** from the **File** menu.

5.3 Print preview

The preview is shown in figure 5.7.

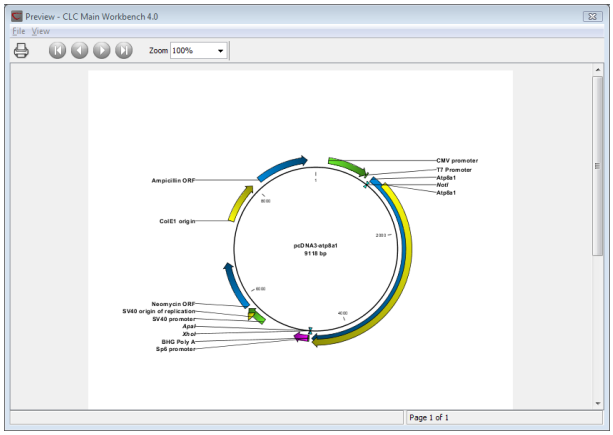

Figure 5.7: *Print preview.*

The **Print preview** window lets you see the layout of the pages that are printed. Use the arrows in the toolbar to navigate between the pages. Click Print ( ) to show the print dialog, which lets you choose e.g. which pages to print.

The **Print preview** window is for preview only - the layout of the pages must be adjusted in the **Page setup**.

Chapter 6

Import/export of data and graphics

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CLC Sequence Viewer handles a large number of different data formats. In order to work with data in the Workbench, it has to be imported ( ). Data types that are not recognized by the Workbench are imported as "external files" which means that when you open these, they will open in the default application for that file type on your computer (e.g. Word documents will open in Word).

This chapter first deals with importing and exporting data in bioinformatic data formats and as external files. Next comes an explanation of how to export graph data points to a file, and how to export graphics.

6.1 Standard import

CLC Sequence Viewer has support for a wide range of bioinformatic data such as molecules, sequences, alignments etc. See a full list of the data formats in section C.1.

These data can be imported through the Import dialog, using drag/drop or copy/paste as explained below.

6.1.1 Import using the import dialog

To start the import using the import dialog: **click Import ( ) in the Toolbar**

This will show a dialog similar to figure 6.1. You can change which kind of file types that should be shown by selecting a file format in the **Files of type** box.

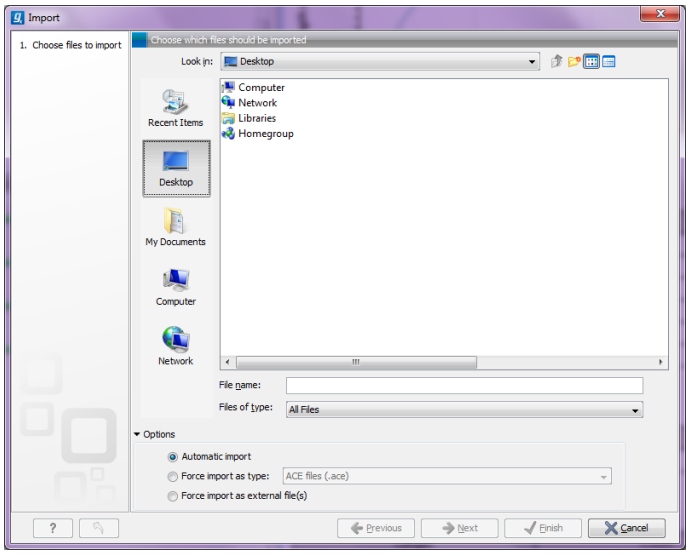

Figure 6.1: *The import dialog.*

Next, select one or more files or folders to import and click **Next**.

This allows you to select a place for saving the result files.

If you import one or more folders, the contents of the folder is automatically imported and placed in that folder in the **Navigation Area**. If the folder contains subfolders, the whole folder structure is imported.

In the import dialog (figure 6.1), there are three import options:

Automatic import This will import the file and *CLC Sequence Viewer* will try to determine the format of the file. The format is determined based on the file extension (e.g. SwissProt files have .swp at the end of the file name) in combination with a detection of elements in the file that are specific to the individual file formats. If the file type is not recognized, it will be imported as an external file. In most cases, automatic import will yield a successful result, but if the import goes wrong, the next option can be helpful:

Force import as type This option should be used if *CLC Sequence Viewer* cannot successfully determine the file format. By forcing the import as a specific type, the automatic determination of the file format is bypassed, and the file is imported as the type specified.

Force import as external file This option should be used if a file is imported as a bioinformatics file when it should just have been external file. It could be an ordinary text file which is imported as a sequence.

6.1.2 Import using drag and drop

It is also possible to drag a file from e.g. the desktop into the **Navigation Area** of *CLC Sequence Viewer*. This is equivalent to importing the file using the **Automatic import** option described above. If the file type is not recognized, it will be imported as an external file.

6.1.3 Import using copy/paste of text

If you have e.g. a text file or a browser displaying a sequence in one of the formats that can be imported by *CLC Sequence Viewer*, there is a very easy way to get this sequence into the **Navigation Area**:

Copy the text from the text file or browser | **Select a folder in the Navigation Area** | **Paste (** **)**

This will create a new sequence based on the text copied. This operation is equivalent to saving the text in a text file and importing it into the *CLC Sequence Viewer*.

If the sequence is not formatted, i.e. if you just have a text like this: "ATGACGAATAGGAGTTC-TAGCTA" you can also paste this into the **Navigation Area**.

Note! Make sure you copy all the relevant text - otherwise *CLC Sequence Viewer* might not be able to interpret the text.

6.1.4 External files

In order to help you organize your research projects, *CLC Sequence Viewer* lets you import all kinds of files. E.g. if you have Word, Excel or pdf-files related to your project, you can import them into the **Navigation Area** of *CLC Sequence Viewer*. Importing an external file creates a copy of the file which is stored at the location you have chosen for import. The file can now be opened by double-clicking the file in the **Navigation Area**. The file is opened using the default application for this file type (e.g. Microsoft Word for .doc-files and Adobe Reader for .pdf).

External files are imported and exported in the same way as bioinformatics files (see section 6.1). Bioinformatics files not recognized by *CLC Sequence Viewer* are also treated as external files.

6.1.5 Import Vector NTI data

There are several ways of importing your Vector NTI data into the CLC Workbench. The best way to go depends on how your data is currently stored in Vector NTI:

- Your data is stored in the Vector NTI Local Database which can be accessed through Vector NTI Explorer. This is described in the first section below.
- Your data is stored as single files on your computer (just like Word documents etc.). This is described in the second section below.

Import from the Vector NTI Local Database

If your Vector NTI data are stored in a Vector NTI Local Database (as the one shown in figure 6.2), you can import all the data in one step, or you can import selected parts of it.

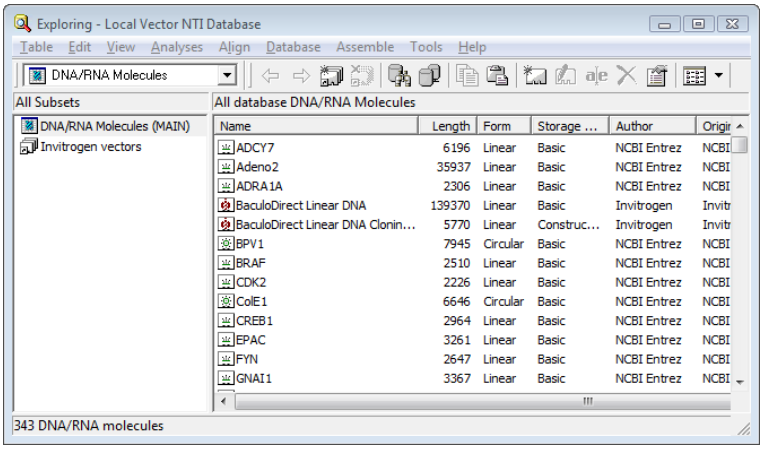
Exploring - Local Vector NTI Database
Table Edit View Analyses Align Database Assemble Tools Help
DNA/RNA Molecules
All Subsets
All database DNA/RNA Molecules
DNA/RNA Molecules (MAIN)
Invitrogen vectors
Name Length Form Storage ... Author
ADCY7 6196 Linear Basic NCBI Entrez
Adeno2 35937 Linear Basic NCBI Entrez
ADRA1A 2306 Linear Basic NCBI Entrez
BaculoDirect Linear DNA 139370 Linear Basic Invitrogen
BaculoDirect Linear DNA Clonin... 5770 Linear Construc... Invitrogen
BPV1 7945 Circular Basic NCBI Entrez
BRAF 2510 Linear Basic NCBI Entrez
CDK2 2226 Linear Basic NCBI Entrez
ColE1 6646 Circular Basic NCBI Entrez
CREB1 2964 Linear Basic NCBI Entrez
EPAC 3261 Linear Basic NCBI Entrez
FYN 2647 Linear Basic NCBI Entrez
GNAI1 3367 Linear Basic NCBI Entrez
343 DNA/RNA molecules

Figure 6.2: *Data stored in the Vector NTI Local Database accessed through Vector NTI Explorer.*

Importing the entire database in one step

From the Workbench, there is a direct import of the whole database (see figure 6.3):

File | Import Vector NTI Database

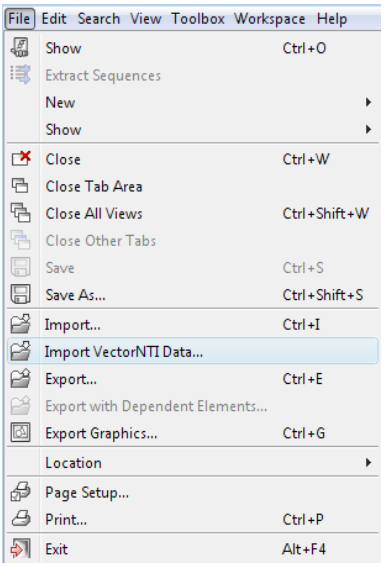

Figure 6.3: *Import the whole Vector NTI Database.*

This will bring up a dialog letting you choose to import from the default location of the database, or you can specify another location. If the database is installed in the default folder, like e.g. *C:\VNTI Database*, press **Yes**. If not, click **No** and specify the database folder manually.

When the import has finished, the data will be listed in the **Navigation Area** of the Workbench as shown in figure 6.4.

If something goes wrong during the import process, please report the problem to support-

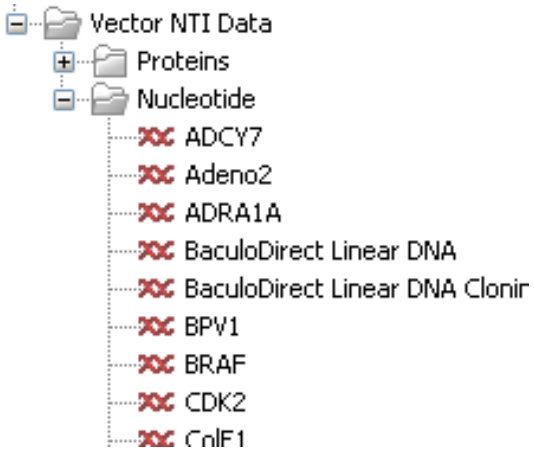

Figure 6.4: *The Vector NTI Data folder containing all imported sequences of the Vector NTI Database.*

clcbio@qiagen.com. To circumvent the problem, see the following section on how to import parts of the database. It will take a few more steps, but you will most likely be able to import this way.

Importing parts of the database

Instead of importing the whole database automatically, you can export parts of the database from Vector NTI Explorer and subsequently import into the Workbench. First, export a selection of files as an archive as shown in figure 6.5.

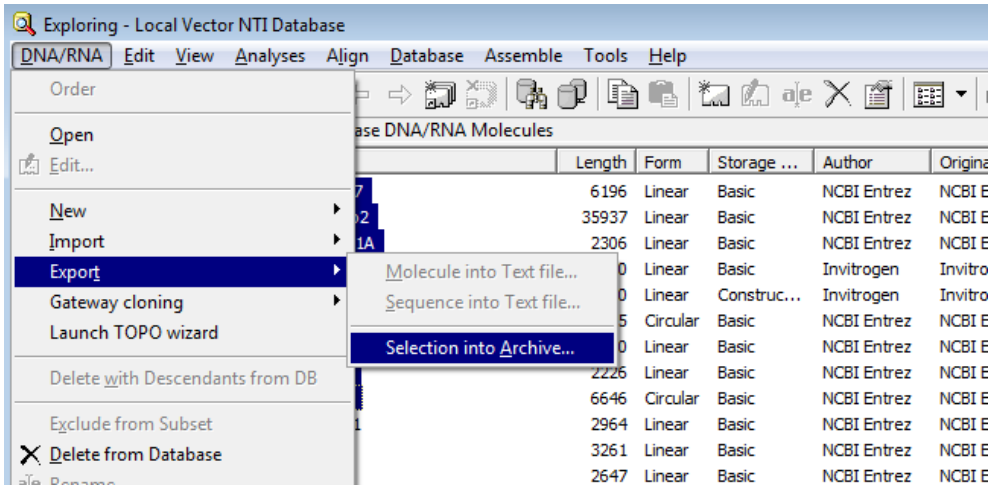

Figure 6.5: *Select the relevant files and export them as an archive through the File menu.*

This will produce a file with a ma4-, pa4- or oa4-extension. Back in the CLC Workbench, click **Import** ( ) and select the file.

Importing single files

In Vector NTI, you can save a sequence in a file instead of in the database (see figure 6.6).

This will give you file with a .gb extension. This file can be easily imported into the CLC Workbench:

Import ( ) | select the file | Select

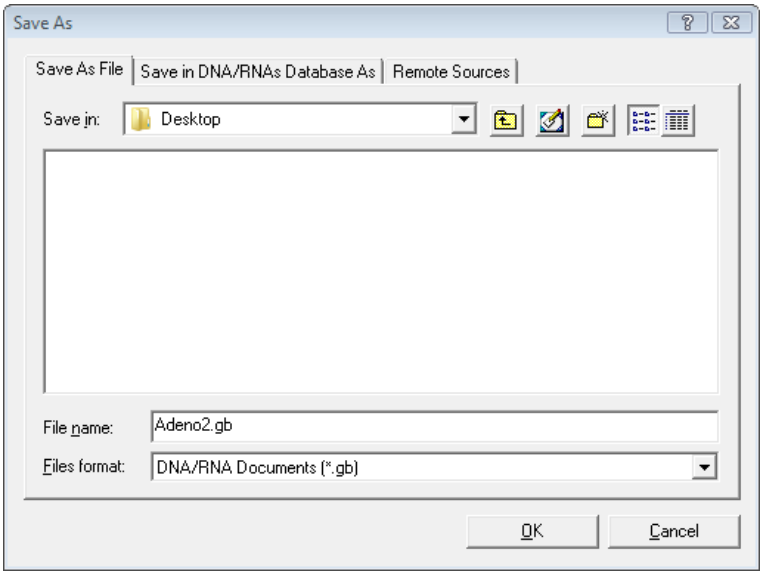

Figure 6.6: *Saving a sequence as a file in Vector NTI.*

You don't have to import one file at a time. You can simply select a bunch of files or an entire folder, and the CLC Workbench will take care of the rest. Even if the files are in different formats.

You can also simply drag and drop the files into the **Navigation Area** of the CLC Workbench.

The CLC Workbench supports import of several NTI formats, but not all. I case problems are encountered, try exporting NTI files to a more generic file format and then import these.

The Vector NTI import is a plugin which is pre-installed in the Workbench. It can be uninstalled and updated using the plugin manager (see section 1.6).

6.2 Data export

The exporter can be used to:

- Export bioinformatic data in most of the formats that can be imported. There are a few exceptions (see section C.1).
- Export one or more data elements at a time to a given format. When multiple data elements are selected, each is written out to an individual file, unless compression is turned on, or "Output as single file" is selected.

The standard export functionality can be launched using the Export button on the toolbar, or by going to the menu:

File | **Export (** **)**

An additional export tool is available from under the File menu:

File | **Export with Dependent Elements**

This tool is described further in section 6.2.2.

The general steps when configuring a standard export job are:

- (Optional) Select the data to export in the **Navigation Area**.
- Start up the exporter tool via the Export button in the toolbar or using the **Export** option under the File menu.
- Select the format the data should be exported to.
- Select the data to export, or confirm the data to export if it was already selected via the **Navigation Area**.
- Configure the parameters. This includes compression, multiple or single outputs, and naming of the output files, along with other format-specific settings where relevant.
- Select where the data should be exported to.
- Click on the button labeled **Finish**.

Selecting data for export - part I. You can select the data elements to export **before** you run the export tool **or after** the format to export to has been selected. If you are not certain which formats are supported for the data being exported, we recommend selecting the data in the **Navigation Area** before launching the export tool.

Selecting a format to export to. When data is pre-selected in the **Navigation Area** before launching the export tool you will see a column in the export interface called **Supported formats**. Formats that the selected data elements can be exported to are indicated by a "Yes" in this column. Supported formats will appear at the top of the list of formats. See figure 6.7.

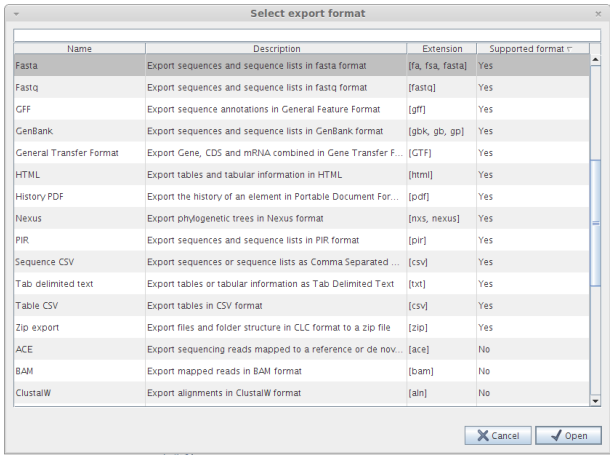

Figure 6.7: *The Select exporter dialog where sequence lists were pre-selected in the Navigation Area before launching the export tool. Here, the formats sequence lists can be exported to are listed at the top, with a Yes in the Selected formats column. Other formats are found below, with No in this column.*

Formats that cannot be used for export of the selected data have a "No" listed in the **Supported formats** column. If you have selected multiple data elements of different types, then formats which can be used for some of the selected data elements but not all of them are indicated by the text "For some elements" in this column.

Please note that the information in the **Supported formats** column only refers to the data already selected in the **Navigation Area**. If you are going to choose your data later in the export process, then the information in this column will not be pertinent.

Only one export format is available if you select a folder to be exported. This is described in more detail in section 6.2.1.

Finding a particular format in the list. You can quickly find a particular format by using the text box at the top of the exporter window as shown in figure 6.8, where formats that include the term VCF are searched for. This search term will remain in place the next time the Export tool is launched. Just delete the text from the search box if you no longer wish only the formats with that term to be listed.

When the desired export format has been identified, click on the button labeled **Open**.

Selecting data for export - part II. A dialog appears, with a name reflecting the format you have chosen. For example if the "Variant Call Format" (VCF format) was selected, the window is labeled "Export VCF".

If you are logged into a CLC Server, you will be asked whether to run the export job using the Workbench or the Server. After this, you are provided with the opportunity to select or de-select data to be exported.

In figure 6.9 we show the selection of a variant track for export to VCF format.

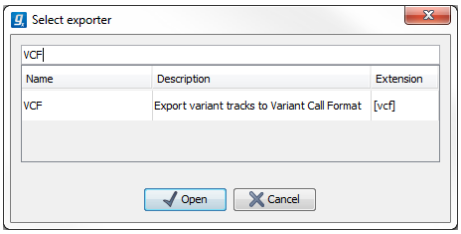

Figure 6.8: *The text field has been used to search for VCF format in the Select exporter dialog.*

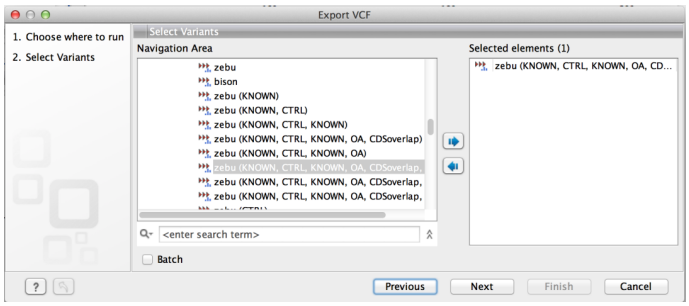

Figure 6.9: *The Select exporter dialog. Select the data element(s) to export.*

The parameters under **Basic export parameters** and **File name** are offered when exporting to any format. There may be additional parameters for particular export formats. This is illustrated here with the VCF exporter, where a reference sequence track must be selected. See figure 6.10.

Compression options. Within the **Basic export parameters** section, you can choose to compress the exported files. The options are no compression (None), gzip or zip format. Choosing zip format results in all data files being compressed into a single file. Choosing gzip compresses the exported file for each data element individually.

Exporting multiple files. If you have selected multiple files of the same type, you can choose to export them in one single file (only for certain file formats) by selecting "Output as single file" in the **Basic export parameters** section. If you wish to keep the files separate after export, make sure this box is not ticked. **Note:** Exporting in zip format will export only one zipped file, but the files will be separated again when unzipped.

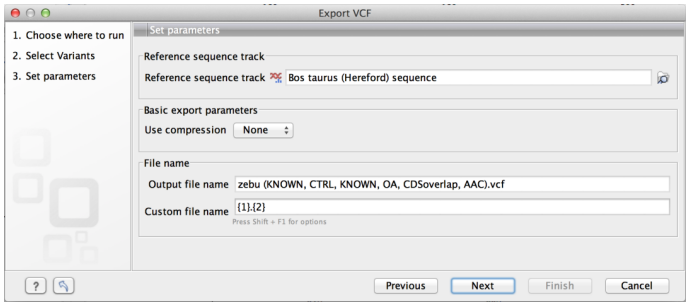

Figure 6.10: *Set the export parameters. When exporting in VCF format, a reference sequence track must be selected.*

Choosing the exported file name(s) The default setting for the **File name** is to use the original data element name as the basename and the export format as the suffix.

When exporting just one data element, or exporting to a zip file, the desired filename could just be typed in the Custom file name box.

When working with the export of multiple files, using some combination of the terms shown by default in this field and in figure 6.12 are recommended. Clicking in the **Custome file name** field with the mouse and then simultaneously pressing the Shift + F1 keys bring up a list of the available terms that can be included in this field. You can see that "{1}" is the name of the input element and "{2}" is the file name extension. It is possible to change the input file name and the file extension name. We will look at an example to illustrate this:

In this example we would like to change the export file format to .fasta in a situation where .fa was the default format that would be used if you kept the default file extension suggestion ("{2}"). To do this replace "{2}" with ".fasta" in the "Custom file name field". You can see that when changing "{2}" to ".fasta" , the file name extension in the "Output file name" field automatically changes to the new format (see figure 6.11).

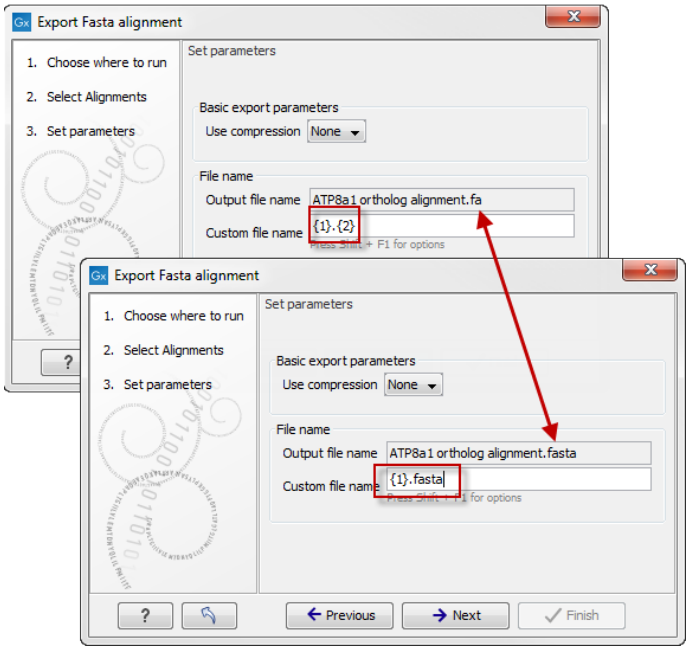

Figure 6.11: *The file name extension can be changed by typing in the preferred file name format.*

As you add or remove text and terms in the **Custome file name** field, the text in the **Output file name** field will change so you can see what the result of your naming choice will be for your data. When working with multiple files, only the name of the first one is shown. Just move the mouse cursor over the name shown in the **Output file name** field to show a listing of the all the filenames.

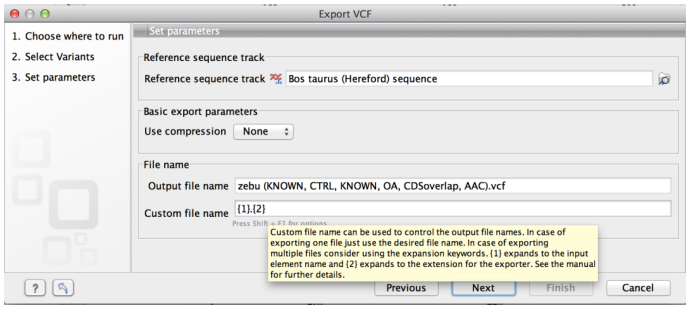
Export VCF
1. Choose where to run
2. Select Variants
3. Set parameters
Set parameters
Reference sequence track
Reference sequence track
Bos taurus (Hereford) sequence
Basic export parameters
Use compression
None
File name
Output file name
zebu (KNOWN, CTRL, KNOWN, OA, CDSoverlap, AAC).vcf
Custom file name
{1}.{2}
Custom file name can be used to control the output file names. In case of exporting one file just use the desired file name. In case of exporting multiple files consider using the expansion keywords. {1} expands to the input element name and {2} expands to the extension for the exporter. See the manual for further details.
Previous
Next
Finish
Cancel

Figure 6.12: *Use the custom file name pattern text field to make custom names.*

The last step is to specify the exported data should be saved (figure 6.13).

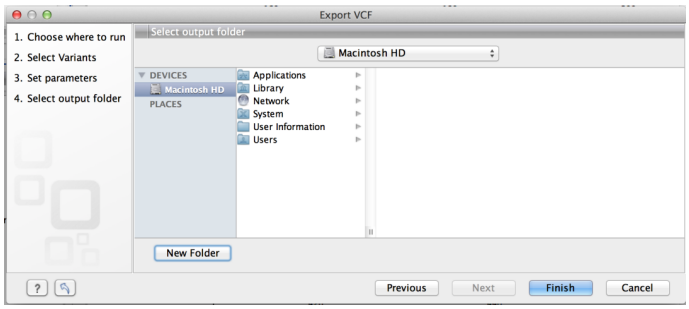

Figure 6.13: *Select where to save the exported data.*

A note about decimals and Locale settings. When exporting to CSV and tab delimited files, decimal numbers are formatted according to the Locale setting of the Workbench (see section 4.1). If you open the CSV or tab delimited file with spreadsheet software like Excel, you should make sure that both the Workbench and the spreadsheet software are using the same Locale.

6.2.1 Export of folders and multiple elements in CLC format

In the list of export formats presented is one called zip format. Choosing this format means that you wish to export the selected data element(s) or folders to a single, compressed CLC format file. This is useful in cases where you wish to exchange data between workbenches or as part of a simple backup procedure.

A zip file generated this way can be imported directly into a CLC Workbench using the Standard Import tool and leaving the import type as Automatic.

Note! When exporting multiple files, the names will be listed in the "Output file name" text field with only the first file name being visible and the rest being substituted by "...", but will appear in a tool tip if you hover the mouse over that field (figure 6.14).

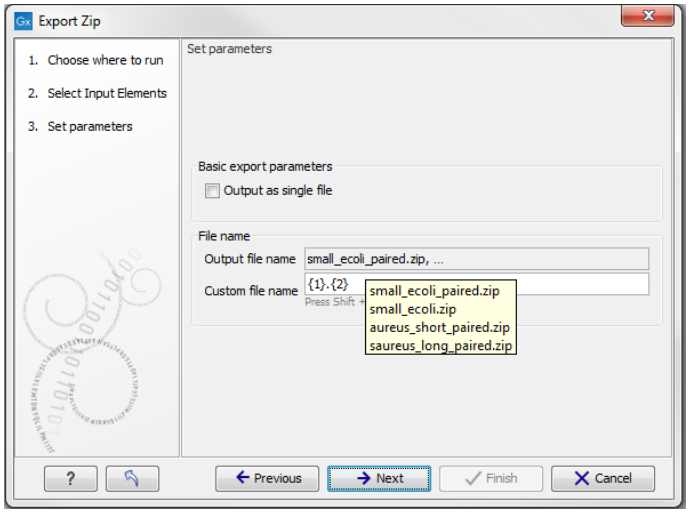

Figure 6.14: *The output file names are listed in the "Output file name" text field.*

6.2.2 Export of dependent elements

Sometimes it can be useful to export the results of an analysis and its dependent elements. That is, the results along with the data that was used in the analysis. For example, one might wish to export an alignment along with all the sequences that were used in generating that alignment.

To export a data element with its dependent elements:

- Select the parent data element (like an alignment) in the **Navigation Area**.
- Start up the exporter tool by going to **File** | **Export with Dependent Elements**.
- Edit the output name if desired and select where the resulting zip format file should be exported to.

The file you export contains compressed CLC format files containing the data element you chose and all its dependent data elements.

A zip file created this way can be imported directly into a CLC workbench by going to

File | **Import** | **Standard Import**

In this case, the import type can be left as Automatic.

6.2.3 Export history

Each data element in the Workbench has a history. The history information includes things like the date and time data was imported or an analysis was run, the parameters and values set, and where the data came from. For example, in the case of an alignment, one would see the sequence data used for that alignment listed. You can view this information for each data element by clicking on the Show History view ( ) at the bottom of the viewing area when a data element is open in the Workbench.

This history information can be exported to a pdf document. To do this:

- (Optional, but preferred) Select the data element (like an alignment) in the **Navigation Area**.

- Start up the exporter tool via the Export button in the toolbar or using the **Export** option under the File menu.
- Select the **History PDF** as the format to export to. See figure 6.15.
- Select the data to export, or confirm the data to export if it was already selected via the **Navigation Area**.
- Edit any parameters of interest, such as the Page Setup details, the output filename(s) and whether or not compression should be applied. See figure 6.16.
- Select where the data should be exported to.
- Click on the button labeled **Finish**.

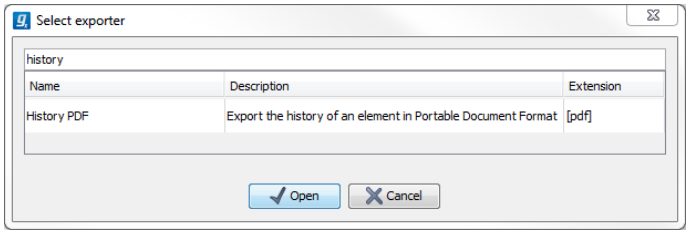

Figure 6.15: *Select "History PDF" for exporting the history of an element.*

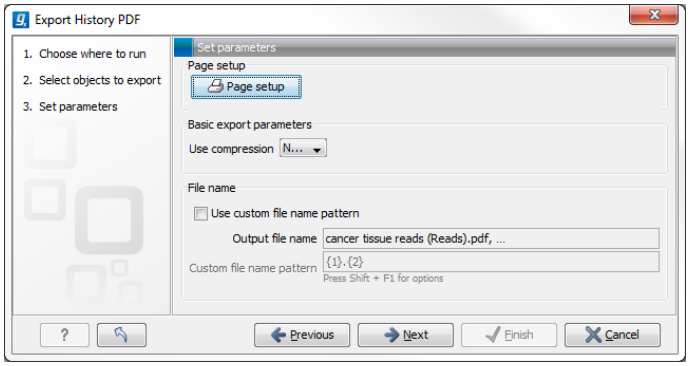

Figure 6.16: *When exporting the history in PDF, it is possible to adjust the page setup.*

6.2.4 The CLC format

The *CLC Sequence Viewer* stores bioinformatic data in CLC format. The CLC format contains data, as well as information about that data like history information and comments you may have added.

A given data element in the Workbench can contain different types of data. This is reflected when exporting data, as the choice of different export formats can lead to the extraction of some parts of that data object rather than others. The part of the data exported reflects the type of data a given format can support. As a simple example, if you export the results of an alignment to Annotation CSV format, you will get just the annotation information. If you exported to Fasta alignment format, you would get the aligned sequences in fasta format, but no annotations.

The CLC format holds all the information for a given data object. Thus if you plan to share the data with colleagues who also have a CLC Workbench or you are communicating with the CLC Support team and you wish to share the data from within the Workbench, exporting to CLC format

is usually the best choice as all information associated with that data object in your Workbench will then be available to the other person who imports that data.

If you are planning to share your data with someone who does not have access to a CLC Workbench, then you will wish to export to another data format. Specifically, one they can use with the software they are working with.

6.2.5 Backing up data from the CLC Workbench

Regular backups of your data are advisable.

The data stored in your CLC Workbench is in the areas defined as CLC Data Locations. Whole data locations can be backed up directly (option 1) or, for smaller amounts of data, you could export the selected data elements to a zip file (option 2).

Option 1: Backing up each CLC Data Location

The easiest way for most people to find out where their data is stored is to put the mouse cursor over the top level directories, that is, the ones that have an icon like ( ), in the **Navigation Area** of the Workbench. This brings up a tool tip with the system location for that data location.

To back up all your CLC data, please ensure that all your CLC Data Locations are backed up.

Here, if you needed to recover the data later, you could put add the data folder from backup as a data location in your Workbench. If the original data location is not present, then the data should be usable directly. If the original data location is still present, the Workbench will re-index the (new) data location. For large volumes of data, re-indexing can take some time.

Information about your data locations can also be found in an xml file called model_settings_300.xml This file is located in the settings folder in the user home area. Further details about this file and how it pertains to data locations in the Workbench can be found in the Deployment Manual:

http://www.clcsupport.com/workbenchdeployment/current/index.php?manual=Changing_default_location.html

Option 2: Export a folder of data or individual data elements to a CLC zip file

This option is for backing up smaller amounts of data, for example, certain results files or a whole data location, where that location contains smaller amounts of data. For data that takes up many gigabases of space, this method can be used, but it can be very demanding on space, as well as time.

Select the data items, including any folders, in the Navigation area of your Workbench and choose to export by going to:

File | **Export (** **)**

and choosing ZIP format.

The zip file created will contain all the data you selected. You can later re-import the zip file into the Workbench by going to:

File | **Import (** **)**

The only data files associated with the *CLC Sequence Viewer* not within a specified data location are BLAST databases. It is unusual to back up BLAST databases as they are usually updated

relatively frequently and in many cases can be easily re-created from the original files or re-downloaded from public resources. If you do wish to backup your BLAST database files, they can be found in the folders specified in the BLAST Database Manager, which is started by going to:

Toolbox | BLAST | Manage BLAST databases .

6.2.6 Export of tables

Tables can be exported in four different formats; CSV, tab-separated, Excel, or html. When exporting a table in CSV, tab-separated, or Excel format, numbers with many decimals are printed in the exported file with 10 decimals, or in 1.123E-5 format when the number is close to zero. When exporting a table in html format, data are exported with the number of decimals that have been defined in the workbench preference settings. When tables are exported in html format from the server or using command line tools, the default number of exported decimals is 3.

The Excel exporters, the CSV and tab delimited exporters, and the HTML exporter have been extended with the ability to export only a sub-set of columns from the object being exported. Uncheck the option "Export all columns" and click next to see a new dialog window in which columns to be exported can be selected (figure 6.17) . The user can choose them one by one or choose a predefined subset:

- All: will select all possible columns.
- None: will clear all preselected column.
- Default: will select the columns preselected by default by the software.
- Last export: will select all windows that were selected during the last export.
- Active editor (only if an active editor is currently open): the columns selected are the same than in the active editor window.

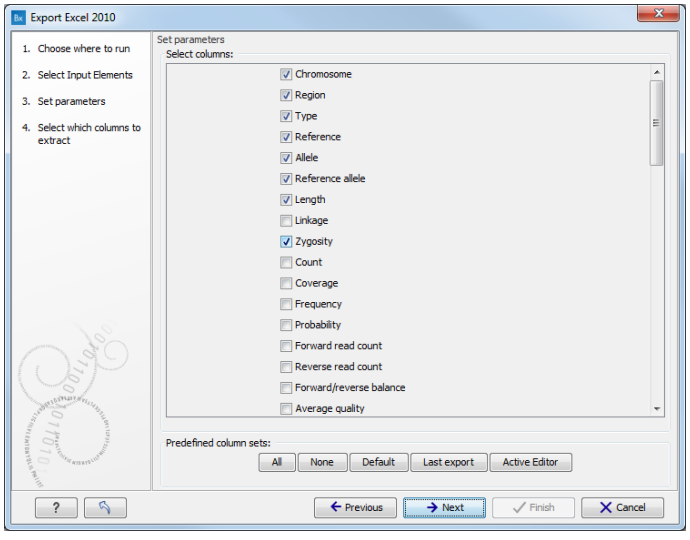

Figure 6.17: *Selecting columns to be exported.*

After selecting columns, the user will be directed to the output destination wizard page.

6.3 Export graphics to files

CLC Sequence Viewer supports export of graphics into a number of formats. This way, the visible output of your work can easily be saved and used in presentations, reports etc. The **Export Graphics** function ( ) is found in the **Toolbar**.

CLC Sequence Viewer uses a WYSIWYG principle for graphics export: What You See Is What You Get. This means that you should use the options in the Side Panel to change how your data, e.g. a sequence, looks in the program. When you export it, the graphics file will look exactly the same way.

It is not possible to export graphics of elements directly from the **Navigation Area**. They must first be opened in a view in order to be exported. To export graphics of the contents of a view:

select tab of View | Graphics ( ) on Toolbar

This will display the dialog shown in figure 6.18.

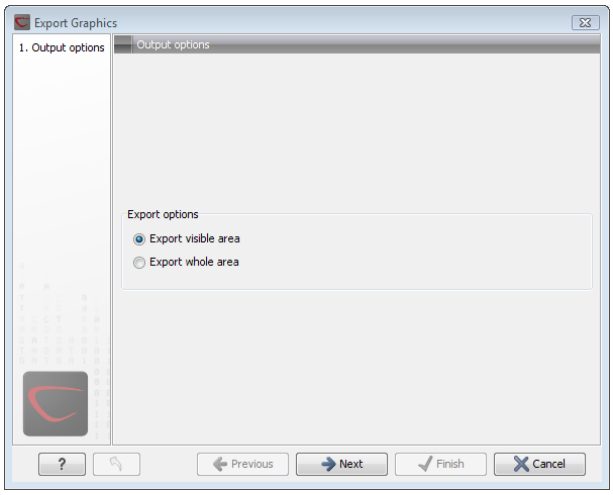

Figure 6.18: *Selecting to export whole view or to export only the visible area.*

6.3.1 Which part of the view to export

In this dialog you can choose to:

- **Export visible area**, or
- **Export whole view**

These options are available for all views that can be zoomed in and out. In figure 6.19 is a view of a circular sequence which is zoomed in so that you can only see a part of it.

When selecting **Export visible area**, the exported file will only contain the part of the sequence that is *visible* in the view. The result from exporting the view from figure 6.19 and choosing **Export visible area** can be seen in figure 6.20.

On the other hand, if you select **Export whole view**, you will get a result that looks like figure 6.21. This means that the graphics file will also include the part of the sequence which is not visible when you have zoomed in.

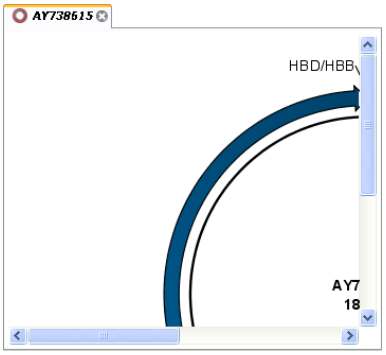

Figure 6.19: *A circular sequence as it looks on the screen.*

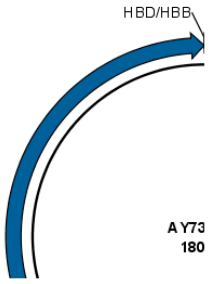

Figure 6.20: *The exported graphics file when selecting Export visible area.*

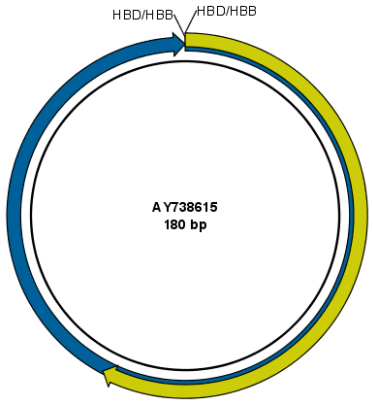

Figure 6.21: *The exported graphics file when selecting Export whole view. The whole sequence is shown, even though the view is zoomed in on a part of the sequence.*

Click **Next** when you have chosen which part of the view to export.

6.3.2 Save location and file formats

In this step, you can choose name and save location for the graphics file (see figure 6.22).

CLC Sequence Viewer supports the following file formats for graphics export:

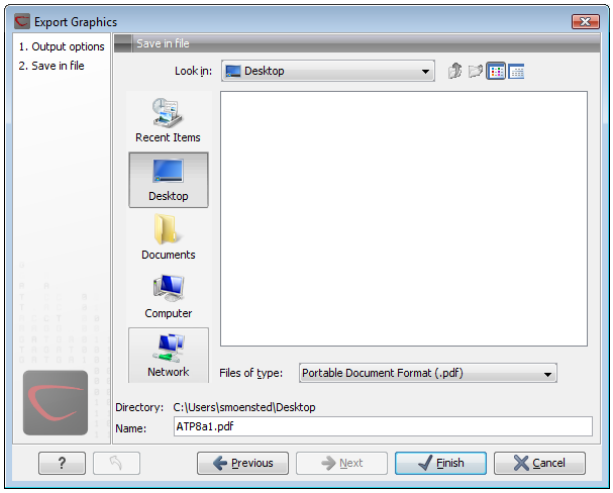

Figure 6.22: *Location and name for the graphics file.*

Format	Suffix	Type
Portable Network Graphics	.png	bitmap
JPEG	.jpg	bitmap
Tagged Image File	.tif	bitmap
PostScript	.ps	vector graphics
Encapsulated PostScript	.eps	vector graphics
Portable Document Format	.pdf	vector graphics
Scalable Vector Graphics	.svg	vector graphics

These formats can be divided into bitmap and vector graphics. The difference between these two categories is described below:

Bitmap images

In a bitmap image, each dot in the image has a specified color. This implies, that if you zoom in on the image there will not be enough dots, and if you zoom out there will be too many. In these cases the image viewer has to interpolate the colors to fit what is actually looked at. A bitmap image needs to have a high resolution if you want to zoom in. This format is a good choice for storing images without large shapes (e.g. dot plots). It is also appropriate if you don't have the need for resizing and editing the image after export.

Vector graphics

Vector graphic is a collection of shapes. Thus what is stored is e.g. information about where a line starts and ends, and the color of the line and its width. This enables a given viewer to decide how to draw the line, no matter what the zoom factor is, thereby always giving a correct image. This format is good for e.g. graphs and reports, but less usable for e.g. dot plots. If the image is to be resized or edited, vector graphics are by far the best format to store graphics. If you open a vector graphics file in an application like e.g. Adobe Illustrator, you will be able to manipulate the image in great detail.

Graphics files can also be imported into the **Navigation Area**. However, no kinds of graphics files can be displayed in *CLC Sequence Viewer*. See section 6.1.4 for more about importing external files into *CLC Sequence Viewer*.

6.3.3 Graphics export parameters

When you have specified the name and location to save the graphics file, you can either click **Next** or **Finish**. Clicking **Next** allows you to set further parameters for the graphics export, whereas clicking **Finish** will export using the parameters that you have set last time you made a graphics export in that file format (if it is the first time, it will use default parameters).

Parameters for bitmap formats

For bitmap files, clicking **Next** will display the dialog shown in figure 6.23.

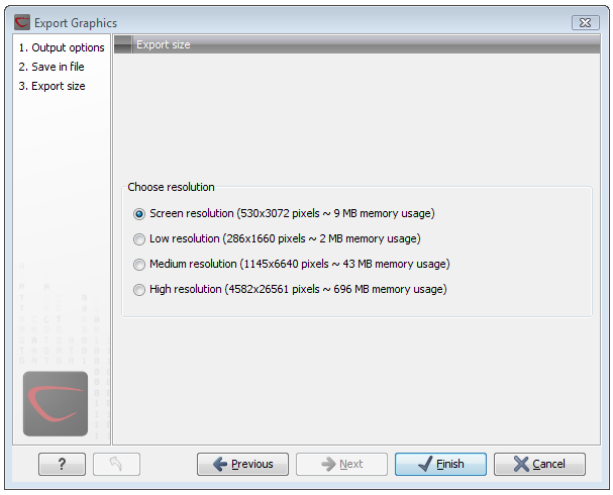
Export Graphics
1. Output options
2. Save in file
3. Export size
Export size
Choose resolution
Screen resolution (530x3072 pixels ~ 9 MB memory usage)
Low resolution (286x1660 pixels ~ 2 MB memory usage)
Medium resolution (1145x6640 pixels ~ 43 MB memory usage)
High resolution (4582x26561 pixels ~ 696 MB memory usage)
Previous
Next
Finish
Cancel

Figure 6.23: *Parameters for bitmap formats: size of the graphics file.*

You can adjust the size (the resolution) of the file to four standard sizes:

- Screen resolution
- Low resolution
- Medium resolution
- High resolution

The actual size in pixels is displayed in parentheses. An estimate of the memory usage for exporting the file is also shown. If the image is to be used on computer screens only, a low resolution is sufficient. If the image is going to be used on printed material, a higher resolution is necessary to produce a good result.

Parameters for vector formats

For pdf format, clicking **Next** will display the dialog shown in figure 6.24 (this is only the case if the graphics is using more than one page).

The settings for the page setup are shown, and clicking the **Page Setup** button will display a dialog where these settings can ba adjusted. This dialog is described in section 5.2.

The page setup is only available if you have selected to export the whole view - if you have chosen to export the visible area only, the graphics file will be on one page with no headers or footers.

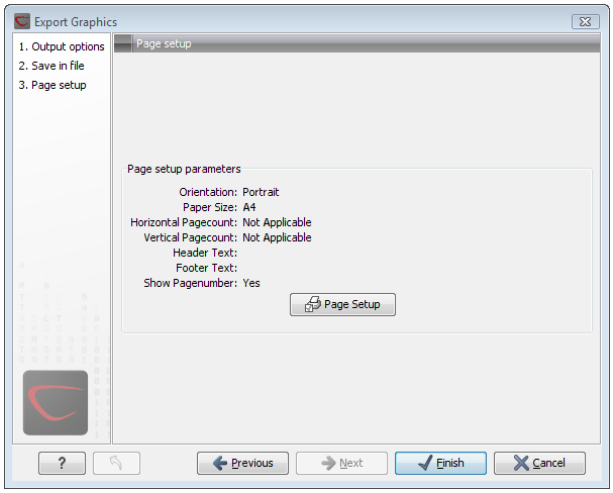

Figure 6.24: *Page setup parameters for vector formats.*

6.3.4 Exporting protein reports

It is possible to export a protein report using the normal **Export** function ( ) which will generate a pdf file with a table of contents:

Click the report in the Navigation Area | Export ( ) in the Toolbar | select pdf

You can also choose to export a protein report using the **Export graphics** function ( ), but in this way you will not get the table of contents.

6.4 Export graph data points to a file

Data points for graphs displayed along the sequence or along an alignment, mapping or BLAST result, can be exported to a semicolon-separated text file (csv format). An example of such a graph is shown in figure 6.25. This graph shows the coverage of reads of a read mapping (produced with *CLC Genomics Workbench*).

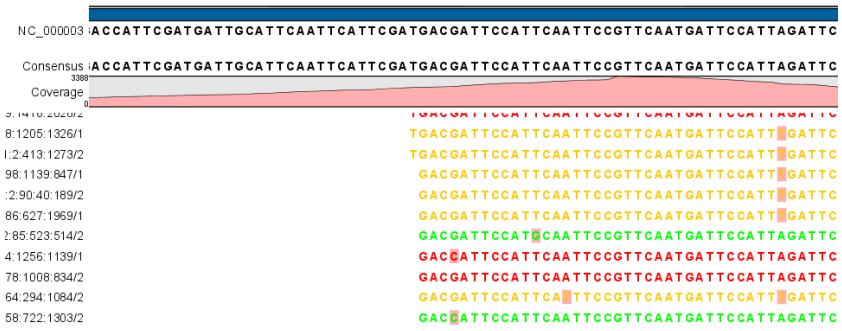

Figure 6.25: *A graph displayed along the mapped reads. Right-click the graph to export the data points to a file.*

To export the data points for the graph, right-click the graph and choose **Export Graph to Comma-separated File**. Depending on what kind of graph you have selected, different options will be shown: If the graph is covering a set of aligned sequences with a main sequence, such as read mappings and BLAST results, the dialog shown in figure 6.26 will be displayed. These kinds of graphs are located under **Alignment info** in the Side Panel. In all other cases, a normal

file dialog will be shown letting you specify name and location for the file.

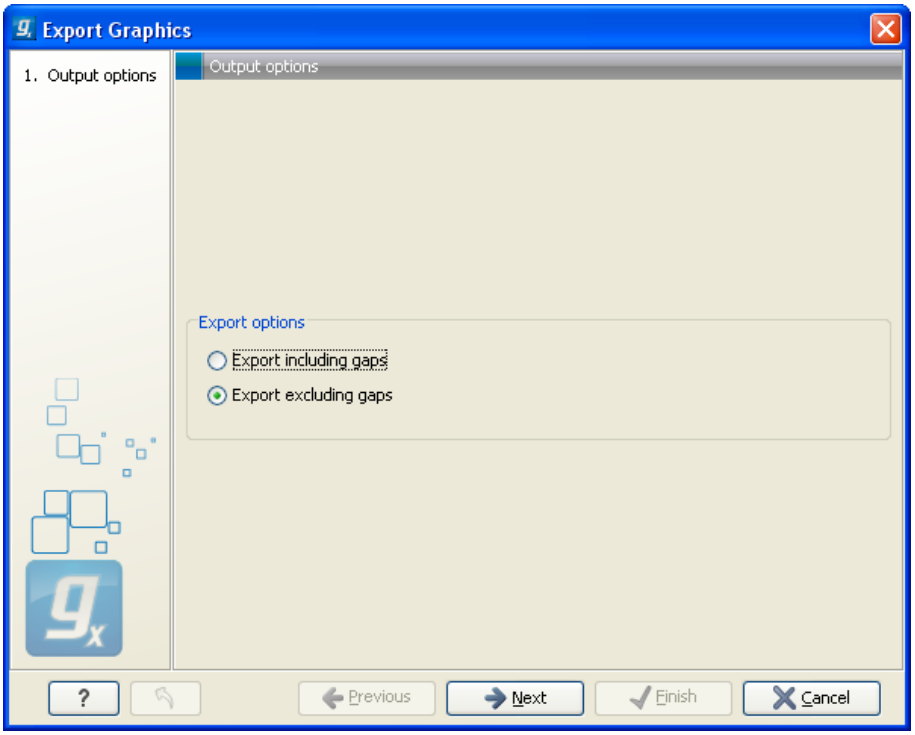

Figure 6.26: *Choosing to include data points with gaps*

In this dialog, select whether you wish to include positions where the main sequence (the reference sequence for read mappings and the query sequence for BLAST results) has gaps. If you are exporting e.g. coverage information from a read mapping, you would probably want to exclude gaps, if you want the positions in the exported file to match the reference (i.e. chromosome) coordinates. If you export including gaps, the data points in the file no longer corresponds to the reference coordinates, because each gap will shift the coordinates.

Clicking **Next** will present a file dialog letting you specify name and location for the file.

The output format of the file is like this:

```
"Position";"Value";
"1";"13";
"2";"16";
"3";"23";
"4";"17";
...
```

6.5 Copy/paste view output

The content of tables, e.g. in reports, folder lists, and sequence lists can be copy/pasted into different programs, where it can be edited. *CLC Sequence Viewer* pastes the data in tabulator separated format which is useful if you use programs like Microsoft Word and Excel. There is a huge number of programs in which the copy/paste can be applied. For simplicity, we include one example of the copy/paste function from a **Folder Content** view to Microsoft Excel.

First step is to select the desired elements in the view:

click a line in the Folder Content view | **hold Shift-button** | **press arrow down/up key**

See figure 6.27.

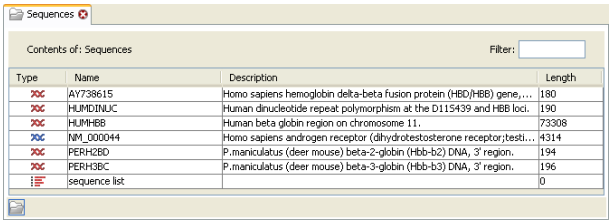

Figure 6.27: *Selected elements in a Folder Content view.*

When the elements are selected, do the following to copy the selected elements:

right-click one of the selected elements | **Edit** | **Copy (** **)**

Then:

right-click in the cell A1 | **Paste (** **)**

The outcome might appear unorganized, but with a few operations the structure of the view in *CLC Sequence Viewer* can be produced. (Except the icons which are replaced by file references in Excel.)

Note that all tables can also be **Exported** ( ) directly in Excel format.

Chapter 7

History log

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CLC Sequence Viewer keeps a log of all operations you make in the program. If e.g. you rename a sequence, align sequences, create a phylogenetic tree or translate a sequence, dock a ligand, align sequences, or create a phylogenetic tree, you can always go back and check what you have done. In this way, you are able to document and reproduce previous operations.

This can be useful in several situations: It can be used for documentation purposes, where you can specify exactly how your data has been created and modified. It can also be useful if you return to a project after some time and want to refresh your memory on how the data was created. Also, if you have performed an analysis and you want to reproduce the analysis on another element, you can check the history of the analysis which will give you all parameters you set.

This chapter will describe how to use the **History** functionality of *CLC Sequence Viewer*.

7.1 Element history

You can view the history of all elements in the **Navigation Area** except files that are opened in other programs (e.g. Word and pdf-files). The history starts when the element appears for the first time in *CLC Sequence Viewer*. To view the history of an element:

Select the element in the Navigation Area | **Show (** **) in the Toolbar** | **History (** **)**

or **If the element is already open** | **History (** **) at the bottom left part of the view**

This opens a view that looks like the one in figure 7.1.

When an element's history is opened, the newest change is submitted in the top of the view. The following information is available:

- **Title**. The action that the user performed.
- **Date and time**. Date and time for the operation. The date and time are displayed according

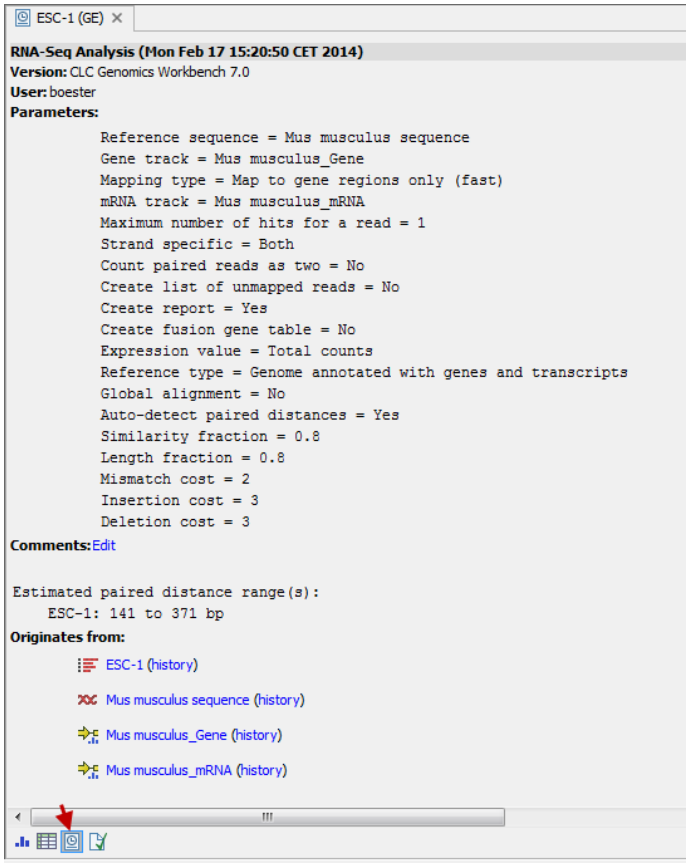
ESC-1 (GE)
RNA-Seq Analysis (Mon Feb 17 15:20:50 CET 2014)
Version: CLC Genomics Workbench 7.0
User: boester
Parameters:
Reference sequence = Mus musculus sequence
Gene track = Mus musculus_Gene
Mapping type = Map to gene regions only (fast)
mRNA track = Mus musculus_mRNA
Maximum number of hits for a read = 1
Strand specific = Both
Count paired reads as two = No
Create list of unmapped reads = No
Create report = Yes
Create fusion gene table = No
Expression value = Total counts
Reference type = Genome annotated with genes and transcripts
Global alignment = No
Auto-detect paired distances = Yes
Similarity fraction = 0.8
Length fraction = 0.8
Mismatch cost = 2
Insertion cost = 3
Deletion cost = 3
Comments: Edit
Estimated paired distance range(s):
ESC-1: 141 to 371 bp
Originates from:
ESC-1 (history)
Mus musculus sequence (history)
Mus musculus_Gene (history)
Mus musculus_mRNA (history)

Figure 7.1: *An element's history.*

to your locale settings (see section 4.1).

- **Version**. The Workbench type and version that has been used.
- **User**. The user who performed the operation. If you import some data created by another person in a CLC Workbench, that person's name will be shown.
- **Parameters**. Details about the action performed. This could be the parameters that were chosen for an analysis.
- **Comments**. By clicking **Edit** you can enter your own comments regarding this entry in the history. These comments are saved.
- **Originates from**. This information is usually shown at the bottom of an element's history. Here, you can see which elements the current element originates from. If you have e.g. created an alignment of three sequences, the three sequences are shown here. Clicking the element selects it in the **Navigation Area**, and clicking the 'history' link opens the element's own history.

7.1.1 Sharing data with history

The history of an element is attached to that element, which means that exporting an element in CLC format (*.clc) will export the history too. In this way, you can share folders and files with others while preserving the history. If an element's history includes source elements (i.e. if

there are elements listed in 'Originates from'), they must also be exported in order to see the full history. Otherwise, the history will have entries named "Element deleted". An easy way to export an element with all its source elements is to use the **Export Dependent Elements** function described in section 6.2.2.

The history view can be printed. To do so, click the **Print** icon ( ). The history can also be exported as a pdf file:

> **Select the element in the Navigation Area | Export ( ) | in "File of type" choose History PDF | Save**

Chapter 8

Batching and result handling

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8.1 How to handle results of analyses

This section will explain how results generated from tools in the Toolbox are handled by *CLC Sequence Viewer*. Note that this also applies to tools not running in batch mode (see above). All the analyses in the **Toolbox** are performed in a step-by-step procedure. First, you select elements for analyses, and then there are a number of steps where you can specify parameters (some of the analyses have no parameters, e.g. when translating DNA to RNA). The final step concerns the handling of the results of the analysis, and it is almost identical for all the analyses so we explain it in this section in general.

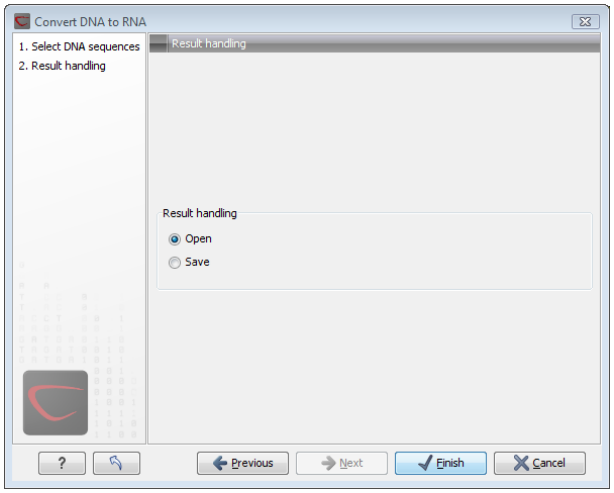


Figure 8.1: *The last step of the analyses exemplified by Translate DNA to RNA.*

In this step, shown in figure 8.1, you have two options:

- **Open.** This will open the result of the analysis in a view. This is the default setting.
- **Save.** This means that the result will not be opened but saved to a folder in the **Navigation Area**. If you select this option, click **Next** and you will see one more step where you can specify where to save the results (see figure 8.2). In this step, you also have the option of creating a new folder or adding a location by clicking the buttons ( )/ ( ) at the top of the dialog.

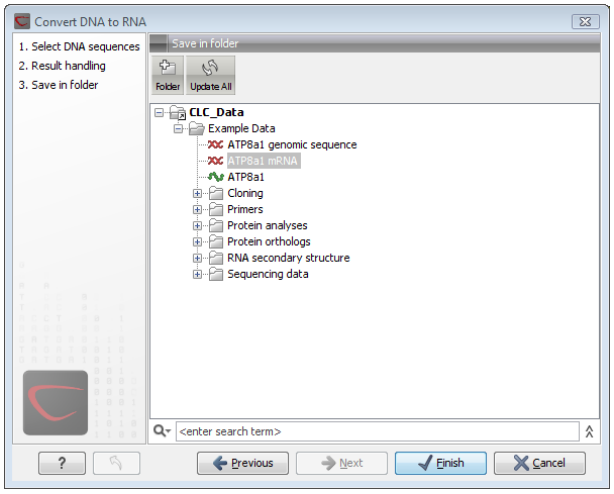


Figure 8.2: *Specify a folder for the results of the analysis.*

8.1.1 Table outputs

Some analyses also generate a table with results, and for these analyses the last step looks like figure 8.3.

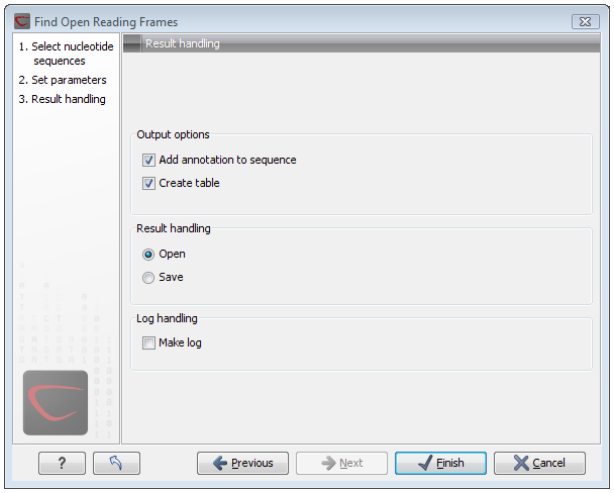


Figure 8.3: *Analyses which also generate tables.*

In addition to the **Open** and **Save** options you can also choose whether the result of the analysis should be added as annotations on the sequence or shown on a table. If both options are

selected, you will be able to click the results in the table and the corresponding region on the sequence will be selected.

If you choose to add annotations to the sequence, they can be removed afterwards by clicking **Undo** ( ) in the **Toolbar**.

8.1.2 Batch log

For some analyses, there is an extra option in the final step to create a log of the batch process (see e.g. figure 8.3). This log will be created in the beginning of the process and continually updated with information about the results. See an example of a log in figure 8.4. In this example, the log displays information about how many open reading frames were found.

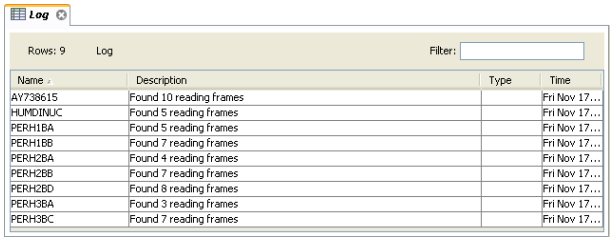

Log
Rows: 9
Log
Filter:
Name
Description
Type
Time
AY738615 Found 10 reading frames Fri Nov 17...
HUMDINUC Found 5 reading frames Fri Nov 17...
PERH1BA Found 5 reading frames Fri Nov 17...
PERH1BB Found 7 reading frames Fri Nov 17...
PERH2BA Found 4 reading frames Fri Nov 17...
PERH2BB Found 7 reading frames Fri Nov 17...
PERH2BD Found 8 reading frames Fri Nov 17...
PERH3BA Found 3 reading frames Fri Nov 17...
PERH3BC Found 7 reading frames Fri Nov 17...

Figure 8.4: *An example of a batch log when finding open reading frames.*

The log will either be saved with the results of the analysis or opened in a view with the results, depending on how you chose to handle the results.

8.2 Working with tables

Tables are used in a lot of places in the *CLC Sequence Viewer*. There are some general features for all tables, irrespective of their contents, that are described here.

Figure 8.5 shows an example of a typical table. This is the table result of **Find Open Reading Frames** ( ). We use this table as an example to illustrate concepts relevant to all kinds of tables.

Table viewing options

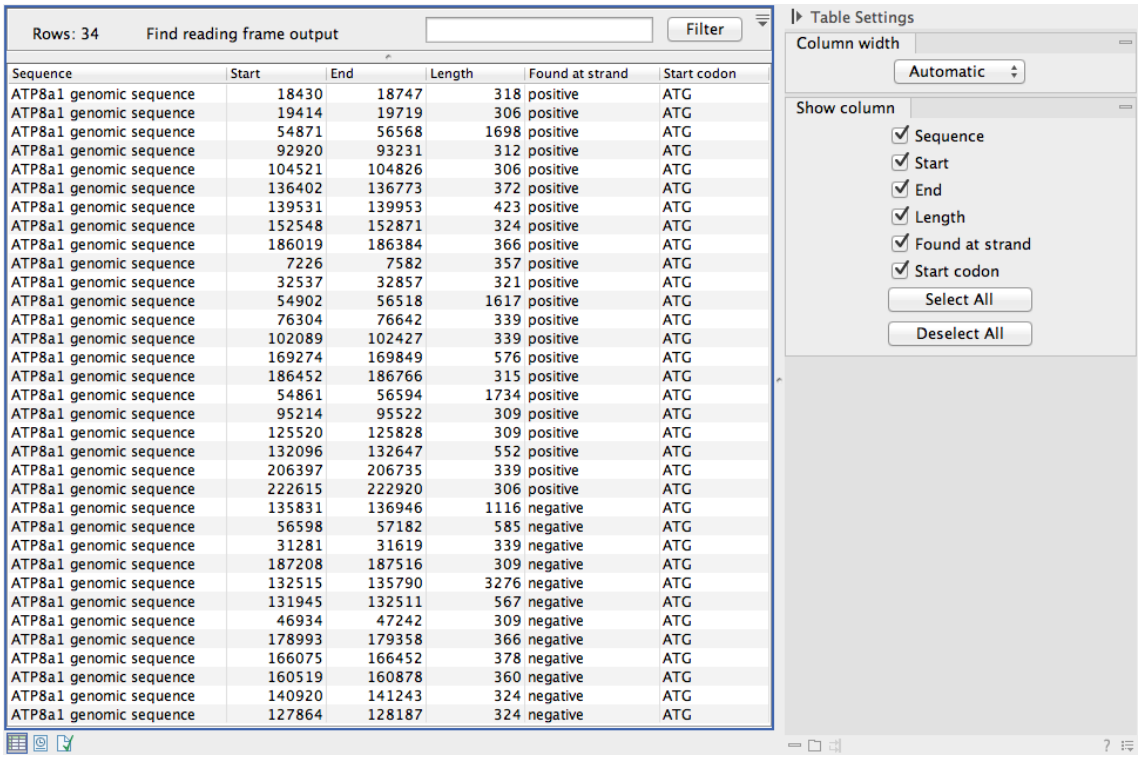
Options relevant to the view of the table can be configured in the **Side Panel** on the right.

For example, the columns that can be dispalyed in the table are listed in the section called **Show column**. The checkboxes allow you to see or hide any of the available columns for that table.

The Column width can be set to **Automatic** or **Manual**. By default, the first time you open a table, it will be set to **Automatic**. The default selected columns are hereby resized to fit the width of the viewing area. When changing to the **Manual** option, column widths will adjust to the actual header size, and each column size can subsequently by adjusted manually. When the table content exceeds the size of the viewing area, a horizontal scroll becomes available for navigation across the columns.

Sorting tables

You can **sort** table according to the values of a particular column by clicking a column header. (Pressing Ctrl - ⌘ on Mac - while you click will refine the existing sorting).



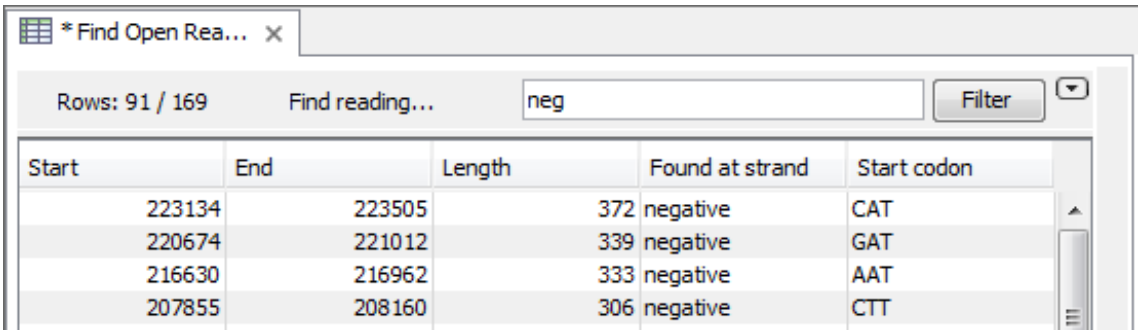
Sequence	Start	End	Length	Found at strand	Start codon
ATP8a1 genomic sequence	18430	18747	318	positive	ATG
ATP8a1 genomic sequence	19414	19719	306	positive	ATG
ATP8a1 genomic sequence	54871	56568	1698	positive	ATG
ATP8a1 genomic sequence	92920	93231	312	positive	ATG
ATP8a1 genomic sequence	104521	104826	306	positive	ATG
ATP8a1 genomic sequence	136402	136773	372	positive	ATG
ATP8a1 genomic sequence	139531	139953	423	positive	ATG
ATP8a1 genomic sequence	152548	152871	324	positive	ATG
ATP8a1 genomic sequence	186019	186384	366	positive	ATG
ATP8a1 genomic sequence	7226	7582	357	positive	ATG
ATP8a1 genomic sequence	32537	32857	321	positive	ATG
ATP8a1 genomic sequence	54902	56518	1617	positive	ATG
ATP8a1 genomic sequence	76304	76642	339	positive	ATG
ATP8a1 genomic sequence	102089	102427	339	positive	ATG
ATP8a1 genomic sequence	169274	169849	576	positive	ATG
ATP8a1 genomic sequence	186452	186766	315	positive	ATG
ATP8a1 genomic sequence	54861	56594	1734	positive	ATG
ATP8a1 genomic sequence	95214	95522	309	positive	ATG
ATP8a1 genomic sequence	125520	125828	309	positive	ATG
ATP8a1 genomic sequence	132096	132647	552	positive	ATG
ATP8a1 genomic sequence	206397	206735	339	positive	ATG
ATP8a1 genomic sequence	222615	222920	306	positive	ATG
ATP8a1 genomic sequence	135831	136946	1116	negative	ATG
ATP8a1 genomic sequence	56598	57182	585	negative	ATG
ATP8a1 genomic sequence	31281	31619	339	negative	ATG
ATP8a1 genomic sequence	187208	187516	309	negative	ATG
ATP8a1 genomic sequence	132515	135790	3276	negative	ATG
ATP8a1 genomic sequence	131945	132511	567	negative	ATG
ATP8a1 genomic sequence	46934	47242	309	negative	ATG
ATP8a1 genomic sequence	178993	179358	366	negative	ATG
ATP8a1 genomic sequence	166075	166452	378	negative	ATG
ATP8a1 genomic sequence	160519	160878	360	negative	ATG
ATP8a1 genomic sequence	140920	141243	324	negative	ATG
ATP8a1 genomic sequence	127864	128187	324	negative	ATG

Figure 8.5: *A table showing the results of an open reading frames analysis.*

Clicking once will sort in ascending order. A second click will change the order to descending. A third click will set the order back its original order.

8.2.1 Filtering tables

The final concept to introduce is **Filtering**. The table filter as an advanced and a simple mode. The simple mode is the default and is applied simply by typing text or numbers (see an example in figure 8.6).[1]



Start	End	Length	Found at strand	Start codon
223134	223505	372	negative	CAT
220674	221012	339	negative	GAT
216630	216962	333	negative	AAT
207855	208160	306	negative	CTT

Figure 8.6: *Typing "neg" in the filter in simple mode.*

Typing "neg" in the filter will only show the rows where "neg" is part of the text in any of the columns (also the ones that are not shown). The text does not have to be in the beginning, thus "ega" would give the same result. This simple filter works fine for fast, textual and non-complicated filtering and searching.

[1]Note that for tables with more than 10000 rows, you have to actually click the **Filter** button for the table to take effect.

However, if you wish to make use of numerical information or make more complex filters, you can switch to the advanced mode by clicking the **Advanced filter** ( ) button. The advanced filter is structure in a different way: First of all, you can have more than one criterion in the filter. Criteria can be added or removed by clicking the **Add** ( ) or **Remove** ( ) buttons. At the top, you can choose whether all the criteria should be fulfilled (**Match all**), or if just one of the needs to be fulfilled (**Match any**).

For each filter criterion, you first have to select which column it should apply to. Next, you choose an operator. For numbers, you can choose between:

- **=** (equal to)
- **<** (smaller than)
- **>** (greater than)
- **<>** (not equal to)
- **abs. value <** (absolute value smaller than. This is useful if it doesn't matter whether the number is negative or positive)
- **abs. value >** (absolute value greater than. This is useful if it doesn't matter whether the number is negative or positive)

Note, that the number of digits displayed is a formatting option which can be set in the View Preferences. The true number may well be (slightly) larger. This behaviour can lead to problems when filtering on exact matches using the **=** (equal to) operator on numbers. Instead, users are advised to use two filters of inequalities (**<** (smaller than) and **>** (greater than)) delimiting a (small) interval around the target value.

For text-based columns, you can choose between:

- **starts with** (the text starts with your search term)
- **contains** (the text does not have to be in the beginning)
- **doesn't contain**
- **=** (the whole text in the table cell has to match, also lower/upper case)
- $\neq$ (the text in the table cell has to not match)
- **is in list** (The text in the table cell has to match one of the items of the list. Items are separated by comma, semicolon, or space. This filter is case-insensitive)

Once you have chosen an operator, you can enter the text or numerical value to use.

If you wish to reset the filter, simply remove ( ) all the search criteria. Note that the last one will not disappear - it will be reset and allow you to start over.

Figure 8.7 shows an example of an advanced filter which displays the open reading frames larger than 400 that are placed on the negative strand.

Both for the simple and the advanced filter, there is a counter at the upper left corner which tells you the number of rows that pass the filter (91 in figure 8.6 and 15 in figure 8.7).

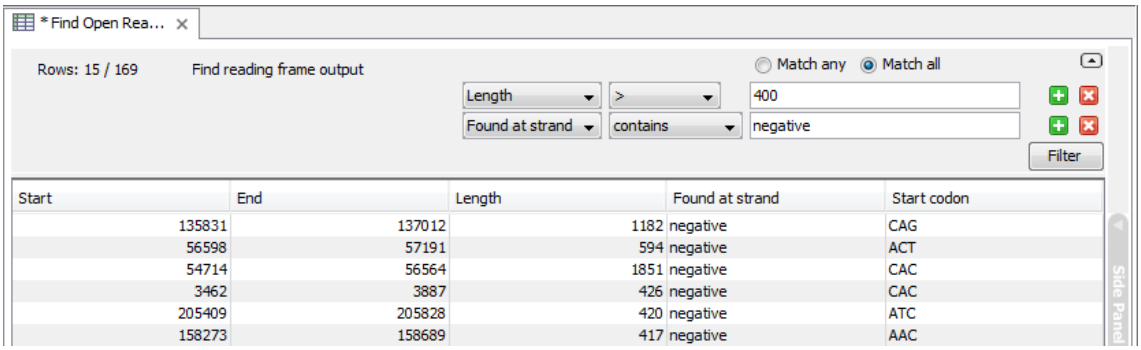


Figure 8.7: *The advanced filter showing open reading frames larger than 400 that are placed on the negative strand.*

Part III

Bioinformatics

Chapter 9

Viewing and editing sequences

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CLC Sequence Viewer offers five different ways of viewing and editing single sequences as described in the first five sections of this chapter. Furthermore, this chapter also explains how to create a new sequence and how to gather several sequences in a sequence list.

9.1 View sequence

When you double-click a sequence in the **Navigation Area**, the sequence will open automatically, and you will see the nucleotides or amino acids. The zoom options described in section 3.3 allow you to e.g. zoom out in order to see more of the sequence in one view. There are a number of options for viewing and editing the sequence which are all described in this section.

All the options described in this section also apply to alignments (further described in section 15.2).

9.1.1 Sequence settings in Side Panel

Each view of a sequence has a **Side Panel** located at the right side of the view (see figure 9.1.

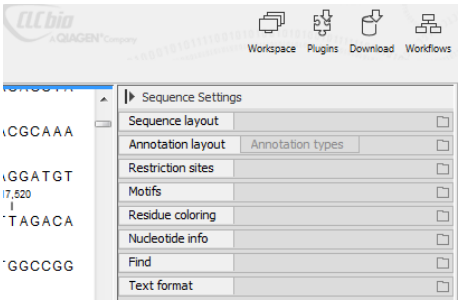

Figure 9.1: *Overview of the Side Panel which is always shown to the right of a view.*

When you make changes in the **Side Panel** the view of the sequence is instantly updated. To show or hide the **Side Panel**:

select the View | Ctrl + U

or **Click the ( ) at the top right corner of the Side Panel to hide | Click the ( ) to the right to show**

Below, each group of settings will be explained. Some of the preferences are not the same for nucleotide and protein sequences, but the differences will be explained for each group of settings.

Note! When you make changes to the settings in the **Side Panel**, they are not automatically saved when you save the sequence. Click **Save/restore Settings** ( ) to save the settings (see section 4.5 for more information).

Sequence Layout

These preferences determine the overall layout of the sequence:

- **Spacing.** Inserts a space at a specified interval:
  - **No spacing.** The sequence is shown with no spaces.
  - **Every 10 residues.** There is a space every 10 residues, starting from the beginning of the sequence.
  - **Every 3 residues, frame 1.** There is a space every 3 residues, corresponding to the reading frame starting at the first residue.
  - **Every 3 residues, frame 2.** There is a space every 3 residues, corresponding to the reading frame starting at the second residue.
  - **Every 3 residues, frame 3.** There is a space every 3 residues, corresponding to the reading frame starting at the third residue.
- **Wrap sequences.** Shows the sequence on more than one line.

  - **No wrap.** The sequence is displayed on one line.
  - **Auto wrap.** Wraps the sequence to fit the width of the view, not matter if it is zoomed in our out (displays minimum 10 nucleotides on each line).
  - **Fixed wrap.** Makes it possible to specify when the sequence should be wrapped. In the text field below, you can choose the number of residues to display on each line.

- **Double stranded.** Shows both strands of a sequence (only applies to DNA sequences).
- **Numbers on sequences.** Shows residue positions along the sequence. The starting point can be changed by setting the number in the field below. If you set it to e.g. 101, the first residue will have the position of -100. This can also be done by right-clicking an annotation and choosing **Set Numbers Relative to This Annotation**.
- **Numbers on plus strand.** Whether to set the numbers relative to the positive or the negative strand in a nucleotide sequence (only applies to DNA sequences).
- **Lock numbers.** When you scroll vertically, the position numbers remain visible. (Only possible when the sequence is not wrapped.)
- **Lock labels.** When you scroll horizontally, the label of the sequence remains visible.
- **Sequence label.** Defines the label to the left of the sequence.
  - Name (this is the default information to be shown).
  - Accession (sequences downloaded from databases like GenBank have an accession number).
  - Latin name.
  - Latin name (accession).
  - Common name.
  - Common name (accession).
- **Matching residues as dots** Residues in aligned sequences identical to residues in the first (reference) sequence will be presented as dots. An option that is only available for "Alignments" and "Read mappings".

Annotation Layout and Annotation Types

See section 9.3.1.

Restriction sites

See section 9.1.2.

Motifs

See section **??**.

Residue coloring

These preferences make it possible to color both the residue letter and set a background color for the residue.

- **Non-standard residues.** For nucleotide sequences this will color the residues that are not C, G, A, T or U. For amino acids only B, Z, and X are colored as non-standard residues.
  - **Foreground color.** Sets the color of the letter. Click the color box to change the color.
  - **Background color.** Sets the background color of the residues. Click the color box to change the color.
- **Rasmol colors.** Colors the residues according to the Rasmol color scheme. See http://www.openrasmol.org/doc/rasmol.html
  - **Foreground color.** Sets the color of the letter. Click the color box to change the color.
  - **Background color.** Sets the background color of the residues. Click the color box to change the color.
- **Polarity colors (only protein).** Colors the residues according to the following categories:
  - **Green** neutral, polar
  - **Black** neutral, nonpolar
  - **Red** acidic, polar
  - **Blue** basic ,polar
  - As with other options, you can choose to set or change the coloring for either the residue letter or its background:
    - **Foreground color.** Sets the color of the letter. Click the color box to change the color.
    - **Background color.** Sets the background color of the residues. Click the color box to change the color.
- **Trace colors (only DNA).** Colors the residues according to the color conventions of chromatogram traces: A=green, C=blue, G=black, and T=red.
  - **Foreground color.** Sets the color of the letter.
  - **Background color.** Sets the background color of the residues.

Find

The Find function can be used for searching the sequence and is invoked by pressing Ctrl + Shift + F (⌘ + Shift + F on Mac). Initially, specify the 'search term' to be found, select the type of search (see various options in the following) and finally click on the Find button. The first occurrence of the search term will then be highlighted. Clicking the find button again will find the next occurrence and so on. If the search string is found, the corresponding part of the sequence will be selected.

- **Search term.** Enter the text or number to search for. The search function does not discriminate between lower and upper case characters.

- **Sequence search.** Search the nucleotides or amino acids. For amino acids, the single letter abbreviations should be used for searching. The sequence search also has a set of advanced search parameters:
  - Include negative strand. This will search on the negative strand as well.
  - Treat ambiguous characters as wildcards in search term. If you search for e.g. ATN, you will find both ATG and ATC. If you wish to find literally exact matches for ATN (i.e. only find ATN - not ATG), this option should not be selected.
  - Treat ambiguous characters as wildcards in sequence. If you search for e.g. ATG, you will find both ATG and ATN. If you have large regions of Ns, this option should not be selected.

  Note that if you enter a position instead of a sequence, it will automatically switch to position search.
- **Annotation search.** Searches the annotations on the sequence. The search is performed both on the labels of the annotations, but also on the text appearing in the tooltip that you see when you keep the mouse cursor fixed. If the search term is found, the part of the sequence corresponding to the matching annotation is selected. Below this option you can choose to search for translations as well. Sequences annotated with coding regions often have the translation specified which can lead to undesired results.
- **Position search.** Finds a specific position on the sequence. In order to find an interval, e.g. from position 500 to 570, enter "500..570" in the search field. This will make a selection from position 500 to 570 (both included). Notice the two periods (..) between the start an end number (see section **??**). If you enter positions including thousands separators like 123,345, the comma will just be ignored and it would be equivalent to entering 123345.
- **Include negative strand.** When searching the sequence for nucleotides or amino acids, you can search on both strands.
- **Name search.** Searches for sequence names. This is useful for searching sequence lists, mapping results and BLAST results.

This concludes the description of the **View Preferences**. Next, the options for selecting and editing sequences are described.

Text format

These preferences allow you to adjust the format of all the text in the view (both residue letters, sequence name and translations if they are shown).

- **Text size.** Five different sizes.
- **Font.** Shows a list of Fonts available on your computer.
- **Bold residues.** Makes the residues bold.

9.1.2 Restriction sites in the Side Panel

Please see section 14.1.

9.1.3 Selecting parts of the sequence

You can select parts of a sequence:

Click Selection ( ) in Toolbar | Press and hold down the mouse button on the sequence where you want the selection to start | move the mouse to the end of the selection while holding the button | release the mouse button

Alternatively, you can search for a specific interval using the find function described above.

If you have made a selection and wish to adjust it:

drag the edge of the selection (you can see the mouse cursor change to a horizontal arrow

or **press and hold the Shift key while using the right and left arrow keys to adjust the right side of the selection.**

If you wish to select the entire sequence:

double-click the sequence name to the left

Selecting several parts at the same time (multiselect)

You can select several parts of sequence by holding down the **Ctrl** button while making selections. Holding down the **Shift** button lets you extend or reduce an existing selection to the position you clicked.

To select a part of a sequence covered by an annotation:

right-click the annotation | Select annotation

or **double-click the annotation**

To select a fragment between two restriction sites that are shown on the sequence:

double-click the sequence between the two restriction sites

(Read more about restriction sites in section 9.1.2.)

Open a selection in a new view

A selection can be opened in a new view and saved as a new sequence:

right-click the selection | Open selection in New View ( )

This opens the annotated part of the sequence in a new view. The new sequence can be saved by dragging the tab of the sequence view into the **Navigation Area**.

The process described above is also the way to manually translate coding parts of sequences (CDS) into protein. You simply translate the new sequence into protein. This is done by:

right-click the tab of the new sequence | Toolbox | Nucleotide Analysis ( )| Translate to Protein ( )

A selection can also be copied to the clipboard and pasted into another program:

make a selection | Ctrl + C (⌘ + C on Mac)

Note! The annotations covering the selection will not be copied.

A selection of a sequence can be edited as described in the following section.

9.1.4 Editing the sequence

When you make a selection, it can be edited by:

right-click the selection | Edit Selection ( )

A dialog appears displaying the sequence. You can add, remove or change the text and click **OK**. The original selected part of the sequence is now replaced by the sequence entered in the dialog. This dialog also allows you to paste text into the sequence using Ctrl + V (⌘ + V on Mac).

If you delete the text in the dialog and press **OK**, the selected text on the sequence will also be deleted. Another way to delete a part of the sequence is to:

right-click the selection | Delete Selection ( )

If you wish to correct only one residue, this is possible by simply making the selection cover only one residue and then type the new residue.

Note When editing annotated nucleotide sequences, the annotation content is not updated automatically (but its position is). Please refer to section **??** for details on annotation editing. Before exporting annotated nucleotide sequences in GenBank format, ensure that the annotations in the Annotations Table reflect the edits that have been made to the sequence.

9.1.5 Sequence region types

The various annotations on sequences cover parts of the sequence. Some cover an interval, some cover intervals with unknown endpoints, some cover more than one interval etc. In the following, all of these will be referred to as *regions*. Regions are generally illustrated by markings (often arrows) on the sequences. An arrow pointing to the right indicates that the corresponding region is located on the positive strand of the sequence. Figure 9.2 is an example of three regions with separate colors.

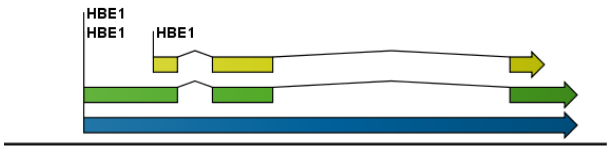

Figure 9.2: *Three regions on a human beta globin DNA sequence (HUMHBB).*

Figure 9.3 shows an artificial sequence with all the different kinds of regions.

9.2 Circular DNA

A sequence can be shown as a circular molecule:

Select a sequence in the Navigation Area and right-click on the file name | Hold the mouse over "Show" to enable a list of options | Select "Circular View" ( )

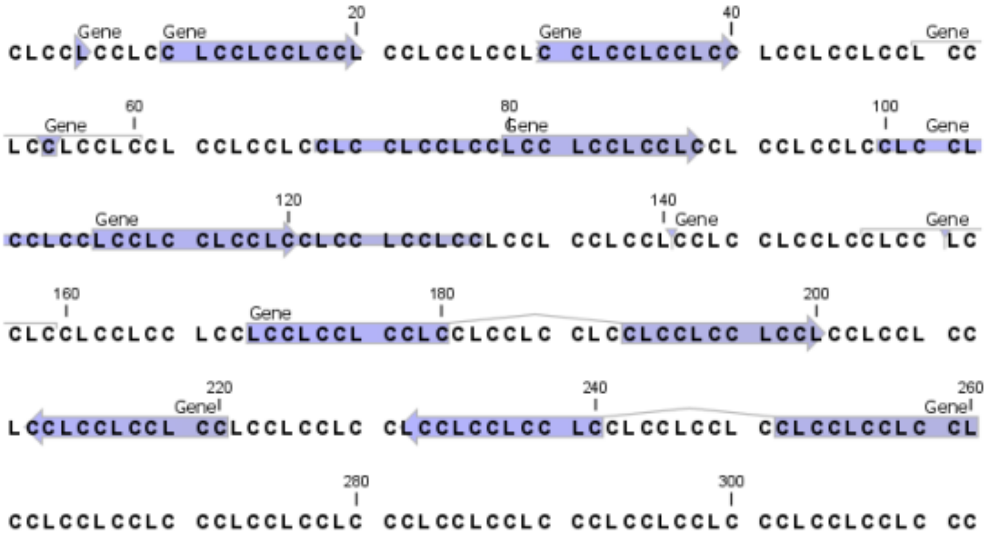

Figure 9.3: *Region #1: A single residue, Region #2: A range of residues including both endpoints, Region #3: A range of residues starting somewhere before 30 and continuing up to and including 40, Region #4: A single residue somewhere between 50 and 60 inclusive, Region #5: A range of residues beginning somewhere between 70 and 80 inclusive and ending at 90 inclusive, Region #6: A range of residues beginning somewhere between 100 and 110 inclusive and ending somewhere between 120 and 130 inclusive, Region #7: A site between residues 140 and 141, Region #8: A site between two residues somewhere between 150 and 160 inclusive, Region #9: A region that covers ranges from 170 to 180 inclusive and 190 to 200 inclusive, Region #10: A region on negative strand that covers ranges from 210 to 220 inclusive, Region #11: A region on negative strand that covers ranges from 230 to 240 inclusive and 250 to 260 inclusive.*

or **If the sequence is already open | Click "Show Circular View" ( ) at the lower left part of the view**

This will open a view of the molecule similar to the one in figure 9.4.

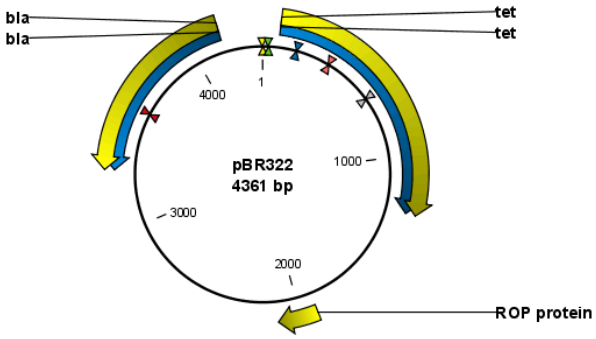

Figure 9.4: *A molecule shown in a circular view.*

This view of the sequence shares some of the properties of the linear view of sequences as described in section 9.1, but there are some differences. The similarities and differences are listed below:

- **Similarities**:
  - The editing options.

- Options for adding, editing and removing annotations.
- **Restriction Sites**, **Annotation Types**, **Find** and **Text Format** preferences groups.

- **Differences**:
  - In the **Sequence Layout** preferences, only the following options are available in the circular view: **Numbers on plus strand**, **Numbers on sequence** and **Sequence label**.
  - You cannot zoom in to see the residues in the circular molecule. If you wish to see these details, split the view with a linear view of the sequence
  - In the **Annotation Layout**, you also have the option of showing the labels as **Stacked**. This means that there are no overlapping labels and that all labels of both annotations and restriction sites are adjusted along the left and right edges of the view.

9.2.1 Using split views to see details of the circular molecule

In order to see the nucleotides of a circular molecule you can open a new view displaying a circular view of the molecule:

> **Press and hold the Ctrl button (⌘ on Mac) | click Show Sequence (ACT) at the bottom of the view**

This will open a linear view of the sequence below the circular view. When you zoom in on the linear view you can see the residues as shown in figure 9.5.

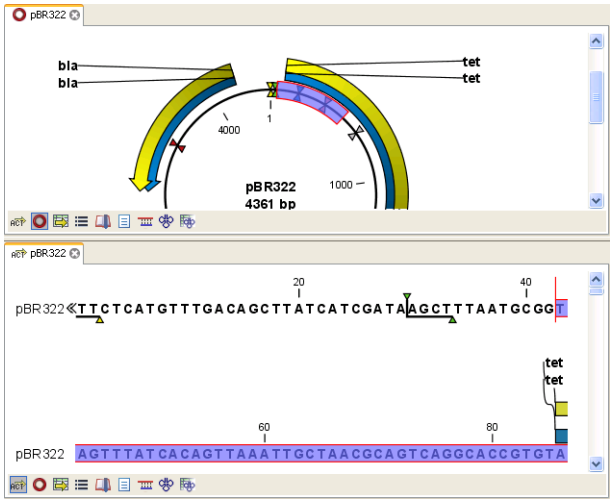

Figure 9.5: *Two views showing the same sequence. The bottom view is zoomed in.*

Note! If you make a selection in one of the views, the other view will also make the corresponding selection, providing an easy way for you to focus on the same region in both views.

9.2.2 Mark molecule as circular and specify starting point

You can mark a DNA molecule as circular by right-clicking its name in either the sequence view or the circular view. In the right-click menu you can also make a circular molecule linear. A circular molecule displayed in the normal sequence view, will have the sequence ends marked with a ï¿½.

The starting point of a circular sequence can be changed by:

make a selection starting at the position that you want to be the new starting point | right-click the selection | Move Starting Point to Selection Start

Note! This can only be done for sequence that have been marked as circular.

9.3 Working with annotations

Annotations provide information about specific regions of a sequence. A typical example is the annotation of a gene on a genomic DNA sequence.

Annotations derive from different sources:

- Sequences downloaded from databases like GenBank are annotated.
- In some of the data formats that can be imported into *CLC Sequence Viewer*, sequences can have annotations (GenBank, EMBL and Swiss-Prot format).
- The result of a number of analyses in *CLC Sequence Viewer* are annotations on the sequence (e.g. finding open reading frames and restriction map analysis).

Note! Annotations are included if you export the sequence in GenBank, Swiss-Prot, EMBL or CLC format. When exporting in other formats, annotations are not preserved in the exported file.

9.3.1 Viewing annotations

Annotations can be viewed in a number of different ways:

- As arrows or boxes in all views displaying sequences (sequence lists, alignments etc)
- In the table of annotations ( ).
- In the text view of sequences ( )

In the following sections, these view options will be described in more detail.

View Annotations in sequence views

Figure 9.6 shows an annotation displayed on a sequence.

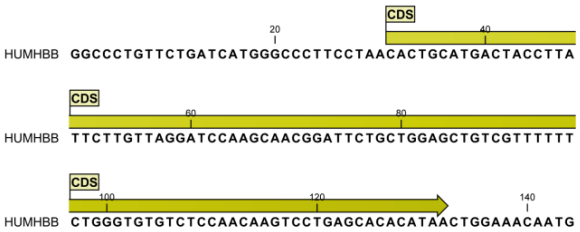

Figure 9.6: *An annotation showing a coding region on a genomic dna sequence.*

The various sequence views listed in section 9.3.1 have different default settings for showing annotations. However, they all have two groups in the **Side Panel** in common:

- **Annotation Layout**
- **Annotation Types**

The two groups are shown in figure 9.7.

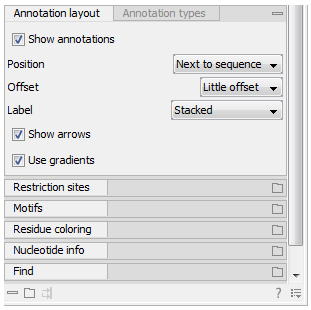

Figure 9.7: *The annotation layout in the Side Panel. The annotation types can be shown by clicking on the "Annotation types" tab.*

In the **Annotation layout** group, you can specify how the annotations should be displayed (notice that there are some minor differences between the different sequence views):

- **Show annotations.** Determines whether the annotations are shown.
- **Position.**
  - **On sequence.** The annotations are placed on the sequence. The residues are visible through the annotations (if you have zoomed in to 100%).
  - **Next to sequence.** The annotations are placed above the sequence.
  - **Separate layer.** The annotations are placed above the sequence and above restriction sites (only applicable for nucleotide sequences).
- **Offset.** If several annotations cover the same part of a sequence, they can be spread out.
  - **Piled.** The annotations are piled on top of each other. Only the one at front is visible.
  - **Little offset.** The annotations are piled on top of each other, but they have been offset a little.
  - **More offset.** Same as above, but with more spreading.
  - **Most offset.** The annotations are placed above each other with a little space between. This can take up a lot of space on the screen.
- **Label.** The name of the annotation can shown as a label. Additional information about the sequence is shown if you place the mouse cursor on the annotation and keep it still.
  - **No labels.** No labels are displayed.
  - **On annotation.** The labels are displayed in the annotation's box.
  - **Over annotation.** The labels are displayed above the annotations.
  - **Before annotation.** The labels are placed just to the left of the annotation.
  - **Flag.** The labels are displayed as flags at the beginning of the annotation.
  - **Stacked.** The labels are offset so that the text of all labels is visible. This means that there is varying distance between each sequence line to make room for the labels.

- **Show arrows.** Displays the end of the annotation as an arrow. This can be useful to see the orientation of the annotation (for DNA sequences). Annotations on the negative strand will have an arrow pointing to the left.
- **Use gradients.** Fills the boxes with gradient color.

In the **Annotation types** group, you can choose which kinds of annotations that should be displayed. This group lists all the types of annotations that are attached to the sequence(s) in the view. For sequences with many annotations, it can be easier to get an overview if you deselect the annotation types that are not relevant.

Unchecking the checkboxes in the **Annotation layout** will not remove this type of annotations them from the sequence - it will just hide them from the view.

Besides selecting which types of annotations that should be displayed, the **Annotation types** group is also used to change the color of the annotations on the sequence. Click the colored square next to the relevant annotation type to change the color.

This will display a dialog with five tabs: Swatches, HSB, HSI, RGB, and CMYK. They represent five different ways of specifying colors. Apply your settings and click **OK**. When you click **OK**, the color settings cannot be reset. The **Reset** function only works for changes made before pressing **OK**.

Furthermore, the **Annotation types** can be used to easily browse the annotations by clicking the small button ( ) next to the type. This will display a list of the annotations of that type (see figure 9.8).

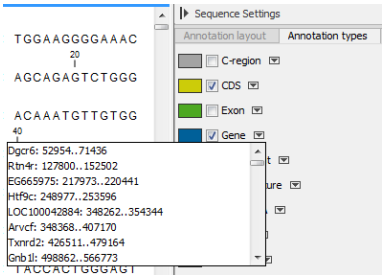

Figure 9.8: *Browsing the gene annotations on a sequence.*

Clicking an annotation in the list will select this region on the sequence. In this way, you can quickly find a specific annotation on a long sequence.

Note: A waved end on an annotation (figure 9.9) means that the annotation is torn, i.e., it extends beyond the sequence displayed.

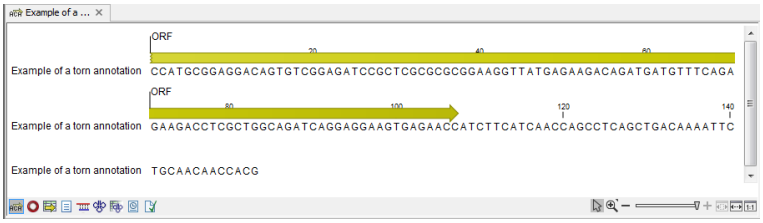

Figure 9.9: *Example of a torn annotation on a sequence.*

View Annotations in a table

Annotations can also be viewed in a table:

Select a sequence in the Navigation Area and right-click on the file name | Hold the mouse over "Show" to enable a list of options | Annotation Table ( )

or **If the sequence is already open | Click Show Annotation Table ( ) at the lower left part of the view**

This will open a view similar to the one in figure 9.10).

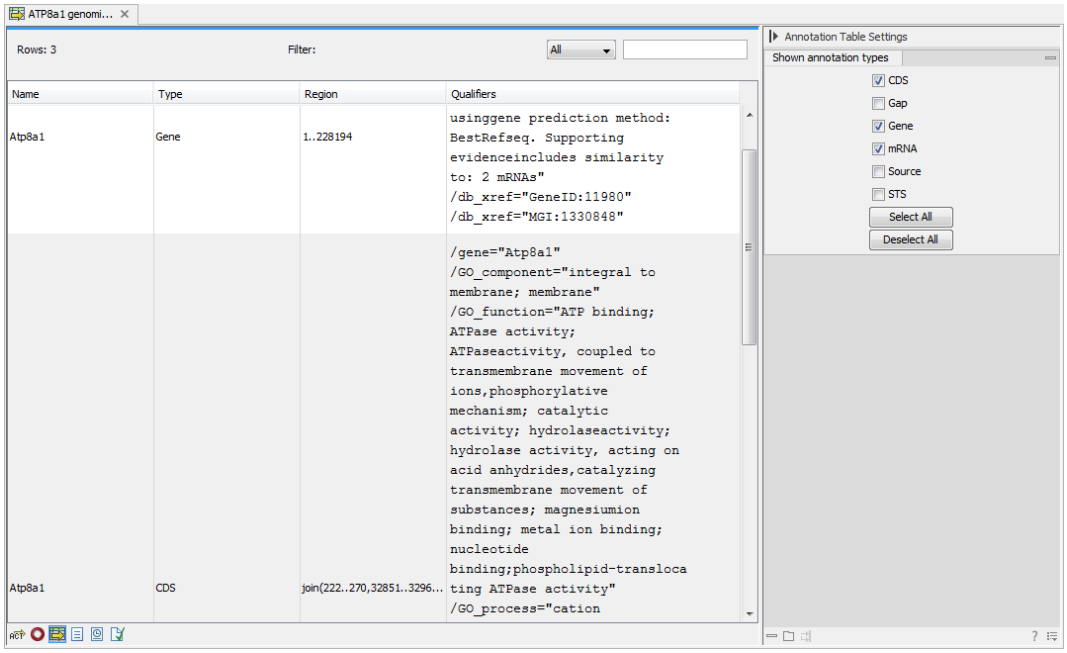

Figure 9.10: *A table showing annotations on the sequence.*

In the **Side Panel** you can show or hide individual annotation types in the table. E.g. if you only wish to see "gene" annotations, de-select the other annotation types so that only "gene" is selected.

Each row in the table is an annotation which is represented with the following information:

- **Name.**
- **Type.**
- **Region.**
- **Qualifiers.**

9.3.2 Removing annotations

Annotations can be hidden using the **Annotation Types** preferences in the **Side Panel** to the right of the view (see section 9.3.1). In order to completely remove the annotation:

right-click the annotation | Delete Annotation ( )

If you want to remove all annotations of one type:

> **right-click an annotation of the type you want to remove | Delete | Delete Annotations of Type "type"**

If you want to remove all annotations from a sequence:

> **right-click an annotation | Delete | Delete All Annotations**

The removal of annotations can be undone using Ctrl + Z or Undo ( ) in the Toolbar.

If you have more sequences (e.g. in a sequence list, alignment or contig), you have two additional options:

> **right-click an annotation | Delete | Delete All Annotations from All Sequences**
>
> **right-click an annotation | Delete | Delete Annotations of Type "type" from All Sequences**

9.4 Element information

The normal view of a sequence (by double-clicking) shows the annotations as boxes along the sequence, but often there is more information available about sequences. This information is available through the **Element info** view.

To view the sequence information:

> **Select a sequence in the Navigation Area and right-click on the file name | Hold the mouse over "Show" to enable a list of options | Element Info ( )**

Another way to show the text view is to open the sequence in the **View Area** and click on the "Show Element Info" icon ( ) found at the bottom of the window.

This will display a view similar to fig 9.11.

Figure 9.11: *The initial display of sequence info for the HUMHBB DNA sequence from the Example data.*

All the lines in the view are headings, and the corresponding text can be shown by clicking the text.

- **Name.** The name of the sequence which is also shown in sequence views and in the

Navigation Area.

- **Description.** A description of the sequence.
- **Comments.** The author's comments about the sequence.
- **Keywords.** Keywords describing the sequence.
- **Db source.** Accession numbers in other databases concerning the same sequence.
- **Gb Division.** Abbreviation of GenBank divisions. See section 3.3 in the GenBank release notes for a full list of GenBank divisions.
- **Length.** The length of the sequence.
- **Modification date.** Modification date from the database. This means that this date does not reflect your own changes to the sequence. See the history (section 7) for information about the latest changes to the sequence after it was downloaded from the database.
- **Latin name.** Latin name of the organism.
- **Common name.** Scientific name of the organism.
- **Taxonomy name.** Taxonomic classification levels.

The information available depends on the origin of the sequence. Sequences downloaded from database like NCBI and UniProt (see section 11) have this information. On the other hand, some sequence formats like fasta format do not contain this information.

Some of the information can be edited by clicking the blue **Edit** text. This means that you can add your own information to sequences that do not derive from databases.

Note that for other kinds of data, the **Element info** will only have **Name** and **Description**.

9.5 View as text

A sequence can be viewed as text without any layout and text formatting. This displays all the information about the sequence in the GenBank file format. To view a sequence as text:

Select a sequence in the Navigation Area and right-click on the file name | Hold the mouse over "Show" to enable a list of options | Select "Text View" ( )

Another way to show the text view is to open the sequence in the **View Area** and click on the "Show Text View" icon ( ) found at the bottom of the window.

This makes it possible to see background information about e.g. the authors and the origin of DNA and protein sequences. Selections or the entire text of the **Sequence Text View** can be copied and pasted into other programs:

Much of the information is also displayed in the **Sequence info**, where it is easier to get an overview (see section 9.4.)

In the **Side Panel**, you find a search field for searching the text in the view.

9.6 Sequence Lists

The **Sequence List** shows a number of sequences in a tabular format or it can show the sequences together in a normal sequence view.

Having sequences in a sequence list can help organizing sequence data.

Sequence lists are generated automatically when you import files containing more than one sequence. Sequence lists may also be created as the output from particular Workbench tool including database searches. See section **??**.

See (chapter 11.1).

Sequence List can also be created from single sequences or by merging already existing sequence lists with the Workbench. To do this:

> **select two or more sequences or sequence lists** | **right-click the elements** | **New** | **Sequence List ( )**

Alternatively, you can launch this took via the menu system:

> **File** | **New** | **Sequence List ( )**

This opens the **Sequence List** Wizard:

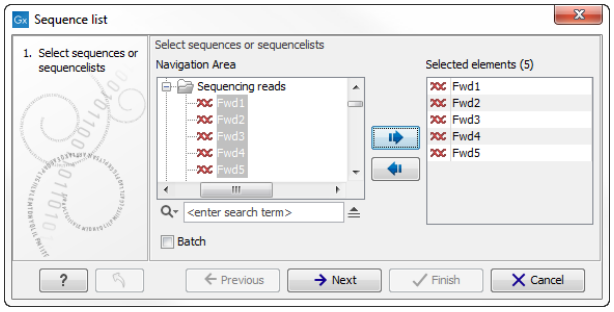

Figure 9.12: *A Sequence List dialog.*

The dialog allows you to select more sequences to include in the list, or to remove already chosen sequences from the list.

Clicking **Finish** opens the sequence list. It can be saved by clicking **Save** ( ) or by dragging the tab of the view into the **Navigation Area**.

Opening a Sequence list is done by:

> **right-click the sequence list in the Navigation Area** | **Show ( )** | **Graphical Sequence List ( ) OR Table ( )**

The two different views of the same sequence list are shown in split screen in figure 9.13.

9.6.1 Graphical view of sequence lists

The graphical view of sequence lists is almost identical to the view of single sequences (see section 9.1). The main difference is that you now can see more than one sequence in the same view.

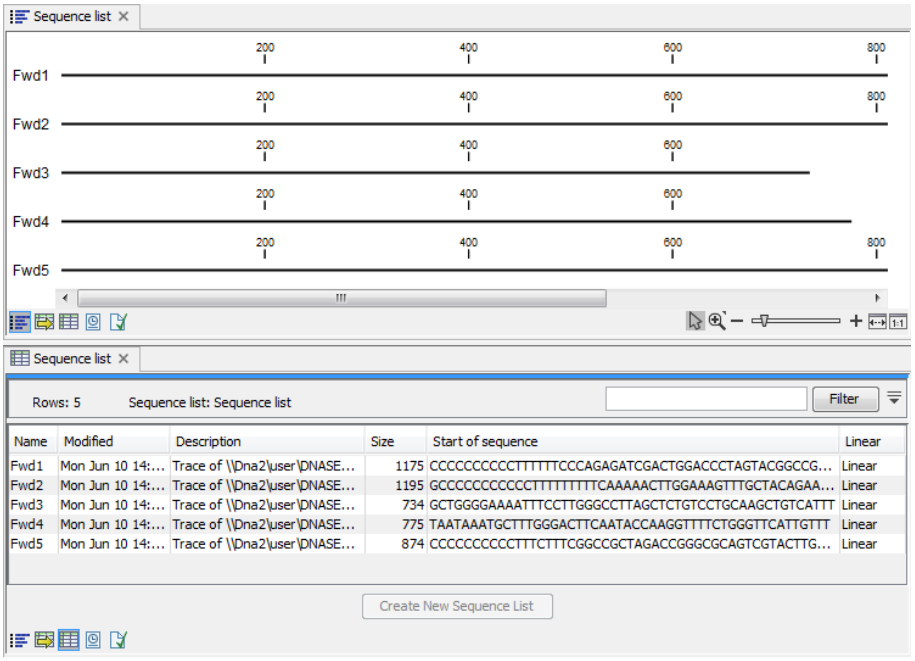
Sequence list
Fwd1
Fwd2
Fwd3
Fwd4
Fwd5
Sequence list
Rows: 5
Sequence list: Sequence list
Filter
Name Modified Description Size Start of sequence Linear
Fwd1 Mon Jun 10 14:... Trace of \\Dna2\user\DNASE... 1175 CCCCCCCCCCTTTTTTCCCAGAGATCGACTGGACCCTAGTACGGCCG... Linear
Fwd2 Mon Jun 10 14:... Trace of \\Dna2\user\DNASE... 1195 GCCCCCCCCCCCTTTTTTTTTCAAAAACTTGGAAAGTTTGCTACAGAA... Linear
Fwd3 Mon Jun 10 14:... Trace of \\Dna2\user\DNASE... 734 GCTGGGGAAAATTTCCTTGGGCCTTAGCTCTGTCCTGCAAGCTGTCATTT Linear
Fwd4 Mon Jun 10 14:... Trace of \\Dna2\user\DNASE... 775 TAATAAATGCTTTGGGACTTCAATACCAAGGTTTTCTGGGTTCATTGTTT Linear
Fwd5 Mon Jun 10 14:... Trace of \\Dna2\user\DNASE... 874 CCCCCCCCCCTTTCTTTCGGCCGCTAGACCGGGCGCAGTCGTACTTG... Linear
Create New Sequence List

Figure 9.13: *A sequence list containing multiple sequences can be viewed in either a table or in a graphical sequence list. The graphical view is useful for viewing annotations and the sequence itself, while the table view provides other information like sequence lengths, and the number of sequences in the list (number of Rows reported).*

However, you also have a few extra options for sorting, deleting and adding sequences:

- To add extra sequences to the list, right-click an empty (white) space in the view, and select **Add Sequences**.
- To delete a sequence from the list, right-click the sequence's name and select **Delete Sequence**.
- To sort the sequences in the list, right-click the name of one of the sequences and select **Sort Sequence List by Name** or **Sort Sequence List by Length**.
- To rename a sequence, right-click the name of the sequence and select **Rename Sequence**.

9.6.2 Sequence list table

Each sequence in the table sequence list is displayed with:

- Name.
- Accession.
- Description.
- Modification date.
- Length.
- First 50 residues.

The number of sequences in the list is reported as the number of Rows at the top of the table view.

Adding and removing sequences from the list is easy: adding is done by dragging the sequence from another list or from the **Navigation Area** and drop it in the table. To delete sequences, simply select them and press **Delete** ( ).

You can also create a subset of the sequence list:

select the relevant sequences | **right-click** | **Create New Sequence List**

This will create a new sequence list, which only includes the selected sequences.

Learn more about tables in Appendix 8.2.

9.6.3 Extract sequences from sequence list

Sequences can be extracted from a sequence list when the sequence list is opened in tabular view. One or more sequences can be dragged (with the mouse) directly from the table into the **Navigation Area**. This allows you to extract specific sequences from the entire list. Another option is to extract all sequences found in the list. This can be done with the **Extract Sequences** tool:

Toolbox | **General Sequence Analysis (** **)**| **Extract Sequences** ( ) .

A description of how to use the **Extract Sequences** tool can be found in section 12.1.

Click **Next** if you wish to adjust how to handle the results (see section 8.1). If not, click **Finish**.

Chapter 10

Viewing structures

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Proteins are amino acid polymers that are involved in all aspects of cellular function. The structure of a protein is defined by its particular amino acid sequence, with the amino acid sequence being referred to as the primary protein structure. The amino acids fold up in local structural elements; helices and sheets, also called the secondary structure of the protein. These structural elements are then packed into globular folds, known as the tertiary structure or the three dimensional structure.

In order to understand protein function it is often valuable to see the three dimensional structure of the protein. This is possible when the structure of the protein has been resolved and published. Structure files are usually deposited in the Protein Data Bank (PDB) `http://www.rcsb.org/`, where the publicly available protein structure files can be searched and downloaded. The vast majority of the protein structures have been determined by X-ray crystallography (88%) while the rest of the structures predominantly have been obtained by Nuclear Magnetic Resonance techniques.

In addition to protein structures, the PDB entries also contain structural information about molecules that interact with the protein, such as nucleic acids, ligands, cofactors, and water. There are also entries, which contain nucleic acids and no protein structure. The **3D Molecule Viewer** in the *CLC Sequence Viewer* is an integrated viewer of such structure files.

The **3D Molecule Viewer** offers a range of tools for inspection and visualization of molecular structures:

- Automatic sorting of molecules into categories: Proteins, Nucleic acids, Ligands, Cofactors, Water molecules
- Hide/unhide individual molecules from the view
- Four different atom-based molecule visualizations
- Backbone visualization for proteins and nucleic acids
- Molecular surface visualization
- Selection of different color schemes for each molecule visualization
- Customized visualization for user selected atoms
- Browse amino acids and nucleic acids from sequence editors started from within the 3D Molecule Viewer

10.1 Importing molecule structure files

Protein Data Bank (PDB) files can be imported from your own file system using Standard Import section 6.1. Molecule Projects exported as CLC objects from other workbenches can also be imported.

10.1.1 Import issues

When opening an imported molecule file for the first time, a notification is briefly shown in the lower left corner of the **Molecule Project** editor, with information of the number of issues encountered during import of the file. The issues are categorized and listed in a table view in the Issues view. The Issues list can be opened by selecting **Show | Issues** from the menu appearing when right-clicking in an empty space in the 3D view (figure 10.1).

Alternatively, the issues can be accessed from the lower left corner of the view, where buttons are shown for each available view. If you hold down the Ctrl key (Cmd on Mac) while clicking on the Issues icon ( ), the list will be shown in a split view together with the 3D view. The issues list is linked with the molecules in the 3D view, such that selecting an entry in the list will select the implicated atoms in the view, and zoom to put them into the center of the 3D view.

10.2 Viewing molecular structures in 3D

An example of a 3D structure that has been opened as a **Molecule Project** is shown in figure 10.2.

10.2.1 Moving and rotating

The molecules can be rotated by holding down the left mouse button while moving the mouse. The right mouse button can be used to move the view.

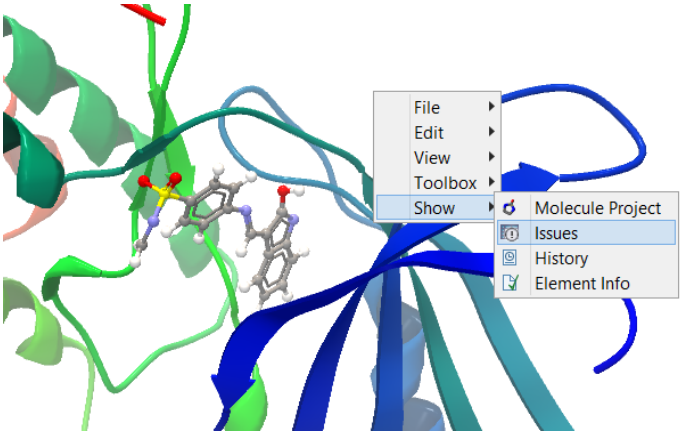

Figure 10.1: *At the bottom of the Molecule Project it is possible to switch to the "Show Issues" view by clicking on the "table-with-exclamation-mark" icon.*

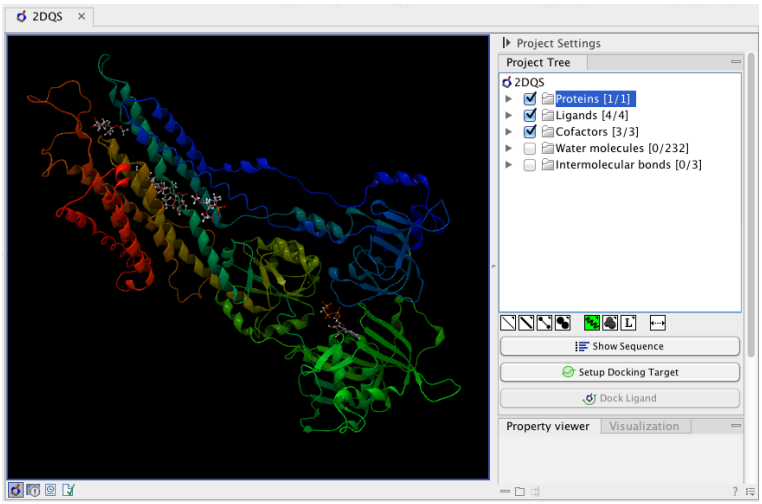

Figure 10.2: *3D view of a calcium ATPase. All molecules in the PDB file are shown in the Molecule Project. The Project Tree in the right side of the window lists the involved molecules.*

Zooming can be done with the scroll-wheel or by holding down both left and right buttons while moving the mouse up and down.

All molecules in the **Molecule Project** are listed in categories in the **Project Tree**. The individual molecules or whole categories can be hidden from the view by un-cheking the boxes next to them.

It is possible to bring a particular molecule or a category of molecules into focus by selecting the molecule or category of interest in the **Project Tree** view and double-click on the molecule or category of interest. Another option is to use the zoom-to-fit button (⇤⇥) at the bottom of the **Project Tree** view.

10.2.2 Troubleshooting 3D graphics errors

The 3D viewer uses OpenGL graphics hardware acceleration in order to provide the best possible experience. If you experience any graphics problems with the 3D view, please make sure that the drivers for your graphics card are up-to-date.

If the problems persist after upgrading the graphics card drivers, it is possible to change to a rendering mode, which is compatible with a wider range of graphic cards. To change the graphics

mode go to Edit in the menu bar, select "Preferences", Click on "View", scroll down to the bottom and find "Molecule Project 3D Editor" and uncheck the box "Use modern OpenGL rendering".

Finally, it should be noted that certain types of visualization are more demanding than others. In particular, using multiple molecular surfaces may result in slower drawing, and even result in the graphics card running out of available memory. Consider creating a single combined surface (by using a selection) instead of creating surfaces for each single object. For molecules with a large number of atoms, changing to wireframe rendering and hiding hydrogen atoms can also greatly improve drawing speed.

10.3 Customizing the visualization

The molecular visualization of all molecules in the Molecule Project can be customized using different visualization styles. The styles can be applied to one molecule at a time, or to a whole category (or a mixture), by selecting the name of either the molecule or the category. Holding down the Ctrl (Cmd on Mac) or shift key while clicking the entry names in the **Project Tree** will select multiple molecules/categories.

The six leftmost quick-style buttons below the **Project Tree** view give access to the molecule visualization styles, while context menus on the buttons (accessible via right-click or left-click-hold) give access to the color schemes available for the visualization styles. Visualization styles and color schemes are also available from context menus directly on the selected entries in the **Project Tree**. Other quick-style buttons are available for displaying hydrogen bonds between Project Tree entries, for displaying labels in the 3D view and for creating custom atom groups. They are all described in detail below.

Note! Whenever you wish to change the visualization styles by right-clicking the entries in the **Project Tree**, please be aware that you must first click on the entry of interest, and ensure it is highlighted in blue, before right-clicking.

10.3.1 Visualization styles and colors

Wireframe, Stick, Ball and stick, Space-filling/CPK

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Four different ways of visualizing molecules by showing all atoms are provided: Wireframe, Stick, Ball and stick, and Space-filling/CPK.

The visualizations are mutually exclusive meaning that only one style can be applied at a time for each selected molecule or atom group.

Six color schemes are available and can be accessed via right-clicking on the quick-style buttons:

- Color by Element. Classic CPK coloring based on atom type (e.g. oxygen red, carbon gray, hydrogen white, nitrogen blue, sulfur yellow).
- Color by Temperature. For PDB files, this is based on the b-factors. For structure models created with tools in a CLC workbench, this is based on an estimate of the local model quality. The color scale goes from blue (0) over white (50) to red (100). The b-factors as well as the local model quality estimate are measures of uncertainty or disorder in the atom position; the higher the number, the higher the uncertainty.

- Color Carbons by Entry. Each entry (molecule or atom group) is assigned its own specific color. Only carbon atoms are colored by the specific color, other atoms are colored by element.
- Color by Entry. Each entry (molecule or atom group) is assigned its own specific color.
- Custom Color. The user selects a molecule color from a palette.
- Custom Carbon Color. The user selects a molecule color from a palette. Only carbon atoms are colored by the specific color, other atoms are colored by element.

Backbone

( )

For the molecules in the Proteins and Nucleic Acids categories, the backbone structure can be visualized in a schematic rendering, highlighting the secondary structure elements for proteins and matching base pairs for nucleic acids. The backbone visualization can be combined with any of the atom-level visualizations.

Five color schemes are available for backbone structures:

- Color by Residue Position. Rainbow color scale going from blue over green to yellow and red, following the residue number.
- Color by Type. For proteins, beta sheets are blue, helices red and loops/coil gray. For nucleic acids backbone ribbons are white while the individual nucleotides are indicated in green (T/U), red (A), yellow (G), and blue (C).
- Color by Backbone Temperature. For PDB files, this is based on the b-factors for the Cα atoms (the central carbon atom in each amino acid). For structure models created with tools in the workbench, this is based on an estimate of the local model quality. The color scale goes from blue (0) over white (50) to red (100). The b-factors as well as the local model quality estimate are measures of uncertainty or disorder in the atom position; the higher the number, the higher the uncertainty.
- Color by Entry. Each chain/molecule is assigned its own specific color.
- Custom Color. The user selects a molecule color from a palette.

Surfaces

( )

Molecular surfaces can be visualized.

Five color schemes are available for surfaces:

- Color by Charge. Charged amino acids close to the surface will show as red (negative) or blue (positive) areas on the surface, with a color gradient that depends on the distance of the charged atom to the surface.

- Color by Element. Smoothed out coloring based on the classic CPK coloring of the heteroatoms close to the surface.
- Color by Temperature. Smoothed out coloring based on the temperature values assigned to atoms close to the surface (See the "Wireframe, Stick, Ball and stick, Space-filling/CPK" section above).
- Color by Entry. Each surface is assigned its own specific color.
- Custom Color. The user selects a surface color from a palette.

A surface spanning multiple molecules can be visualized by creating a custom atom group that includes all atoms from the molecules (see section 10.3.1)

It is possible to adjust the opacity of a surface by adjusting the transparency slider at the bottom of the menu.

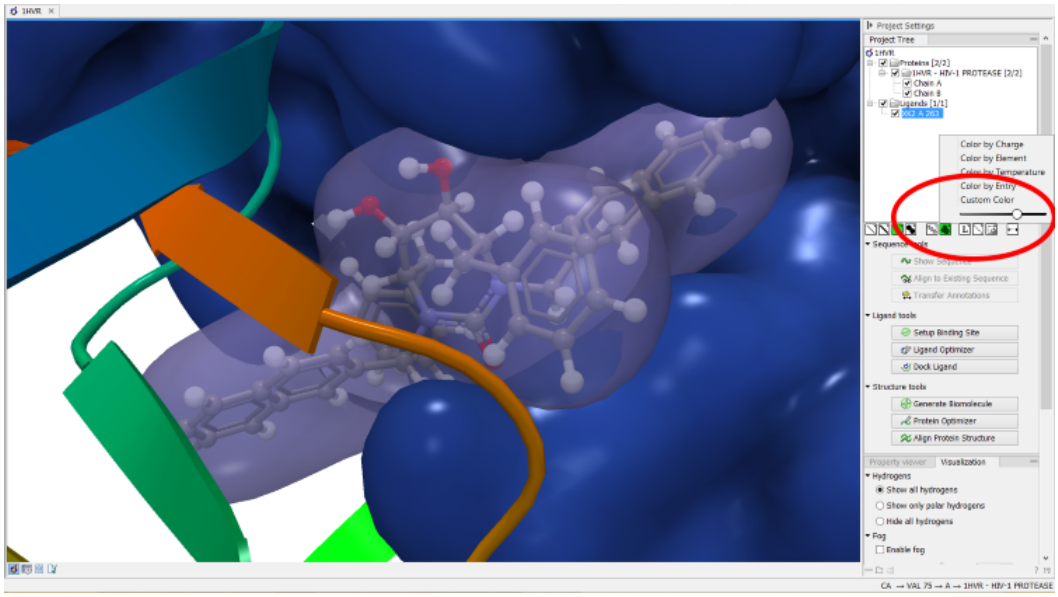

Figure 10.3: *Transparent surfaces*

Notice that visual artifacts may appear when rotating a transparent surface. These artifacts disappear as soon as the mouse is released.

Labels

(L)

Labels can be added to the molecules in the view by selecting an entry in the Project Tree and clicking the label button at the bottom of the Project Tree view. The color of the labels can be adjusted from the context menu by right clicking on the selected entry (which must be highlighted in blue first) or on the label button in the bottom of the Project Tree view (see figure 10.4).

- For proteins and nucleic acids, each residue is labelled with the PDB name and number.
- For ligands, each atom is labelled with the atom name as given in the input.

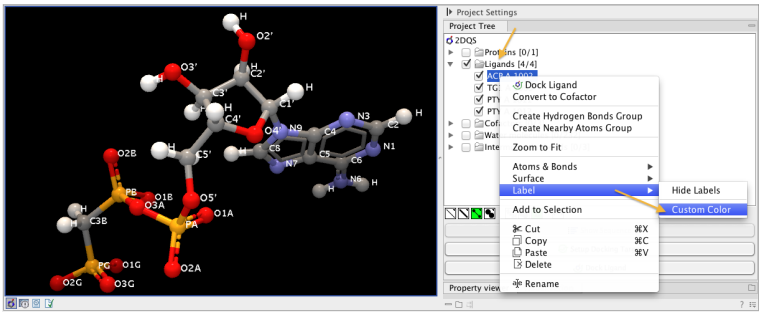

Figure 10.4: *The color of the labels can be adjusted in two different ways. Either directly using the label button by right clicking the button, or by right clicking on the molecule or category of interest in the Project Tree.*

- For cofactors and water, one label is added with the name of the molecule.
- For atom groups including protein atoms, each protein residue is labelled with the PDB name and number.
- For atom groups not including protein atoms, each atom is labelled with the atom name as given in the input.

Labels can be removed again by clicking on the label button.

Hydrogen bonds

( )

The Show Hydrogen Bond visualization style may be applied to molecules and atom group entries in the project tree. If this style is enabled for a project tree entry, hydrogen bonds will be shown to all other currently visible objects. The hydrogen bonds are updated dynamically: if a molecule is toggled off, the hydrogen bonds to it will not be shown.

It is possible to customize the color of the hydrogen bonds using the context menu.

Create atom group

( )

Often it is convenient to use a unique visualization style or color to highlight a particular set of atoms, or to visualize only a subset of atoms from a molecule. This can be achieved by creating an atom group. Atom groups can be created based on atoms selected in the 3D view or entries selected in the Project Tree. When an atom group has been created, it appears as an entry in the Project Tree in the category "Atom groups". The atoms can then be hidden or shown, and the visualization changed, just as for the molecule entries in the Project Tree.

Note that an atom group entry can be renamed. Select the atom group in the Project Tree and invoke the right-click context menu. Here, the Rename option is found.

Create atom group based on atoms selected in 3D view

When atoms are selected in the 3D view, brown spheres indicate which atoms are included in the selection. The selection will appear as the entry "Current" in the Selections category in the Project Tree.

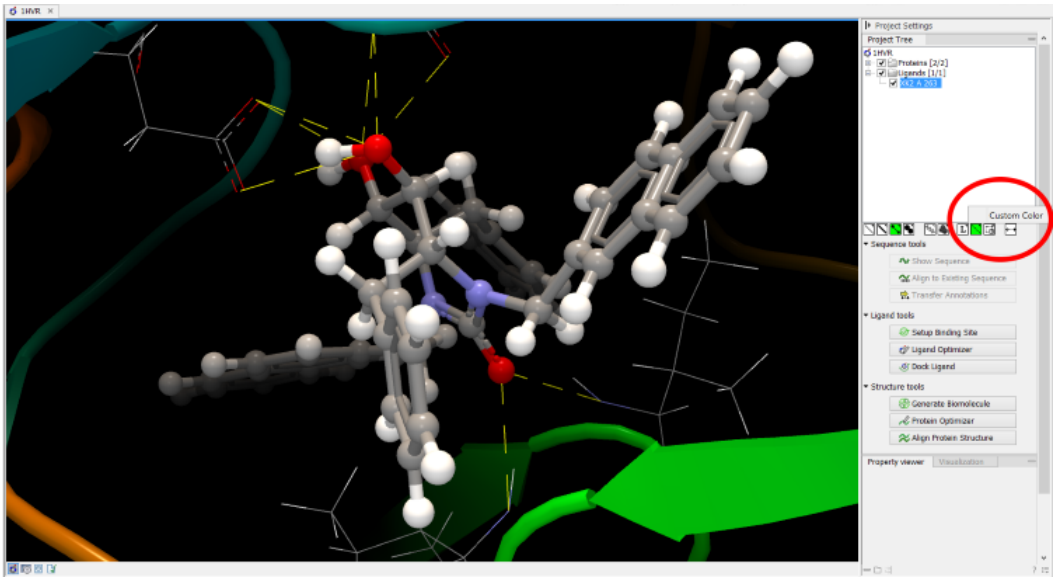

Figure 10.5: *The hydrogen bond visualization setting, with custom bond color*

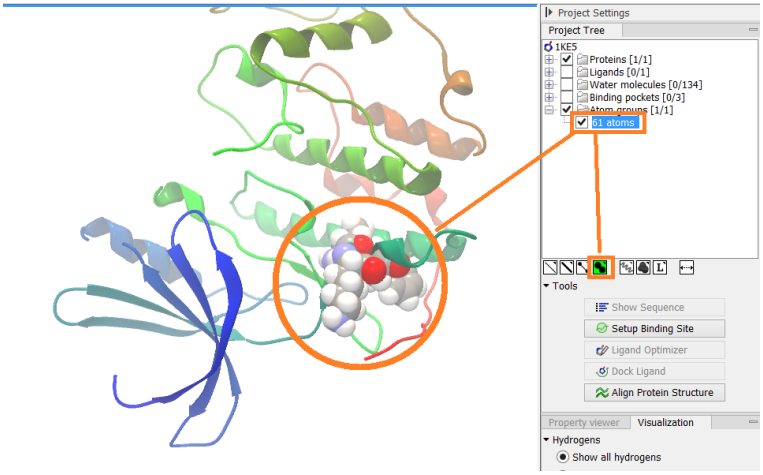

Figure 10.6: *An atom group that has been highlighted by adding a unique visualization style.*

Once a selection has been made, press the "Create Atom Group" button and a context menu will show different options for creating a new atom group based on the selection:

- Selected Atoms. Creates an atom group containing exactly the selected atoms (those indicated by brown spheres). If an entire molecule or residue is selected, this option is not displayed.
- Selected Residue(s)/Molecules. Creates an atom group that includes all atoms in the selected residues (for entries in the protein and nucleic acid categories) and molecules (for the other categories).
- Nearby Atoms. Creates an atom group that contains residues (for the protein and nucleic acid categories) and molecules (for the other categories) within 5 Å of the selected atoms. Only atoms from currently visible Project Tree entries are considered.
- Hydrogen Bonded Atoms. Creates an atom group that contains residues (for the protein and nucleic acid categories) and molecules (for the other categories) that have hydrogen

bonds to the selected atoms. Only atoms from currently visible Project Tree entries are considered.

There are several ways to select atoms in the 3D view:

- Double click to select. Click on an atom to select it. When you double click on an atom that belongs to a residue in a protein or in a nucleic acid chain, the entire residue will be selected. For small molecules, the entire molecule will be selected.
- Adding atoms to a selection. Holding down Ctrl while picking atoms, will pile up the atoms in the selection. All atoms in a molecule or category from the Project Tree, can be added to the "Current" selection by choosing "Add to Current Selection" in the context menu. Similarly, entire molecules can be removed from the current selection via the context menu.
- Spherical selection. Hold down the shift-key, click on an atom and drag the mouse away from the atom. Then a sphere centered on the atom will appear, and all atoms inside the sphere, visualized with one of the all-atom representations will be selected. The status bar (lower right corner) will show the radius of the sphere.
- Show Sequence. Another option is to select protein or nucleic acid entries in the Project Tree, and click the "Show Sequence" button found below the Project Tree (section 10.5.1). A split-view will appear with a sequence editor for each of the sequence data types (Protein, DNA, RNA) (figure 10.7). If you then select residues in the sequence view, the backbone atoms of the selected residues will show up as the "Current" selection in the 3D view and the Project Tree view. Notice that the link between the 3D view and the sequence editor is lost if either window is closed, or if the sequence is modified.

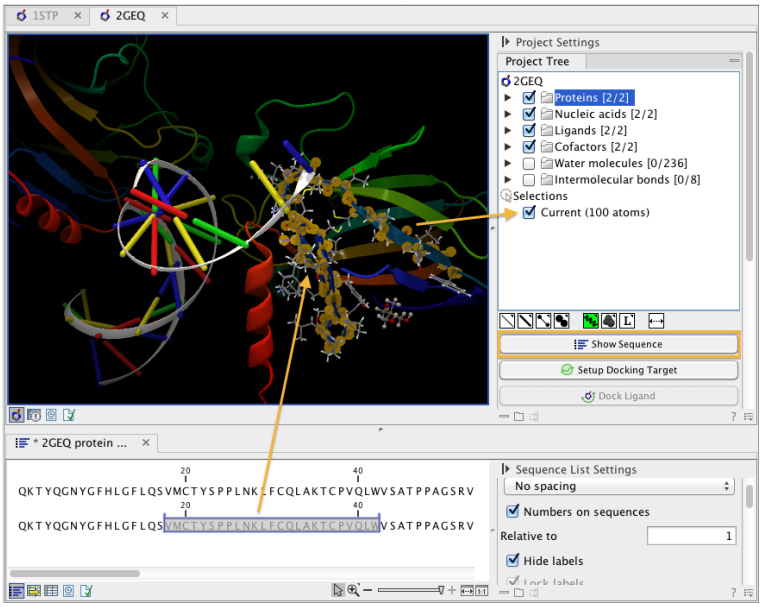

Figure 10.7: *The protein sequence in the split view is linked with the protein structure. This means that when a part of the protein sequence is selected, the same region in the protein structure will be selected.*

Create atom group based on entries selected in the Project Tree

Select one or more entries in the Project Tree, and press the "Create Atom Group" button, then a context menu will show different options for creating a new atom group based on the selected entries:

- Nearby Atoms. Creates an atom group that contains residues (for the protein and nucleic acid categories) and molecules (for the other categories) within 5 Å of the selected entries. Only atoms from currently visible Project Tree entries are considered. This option is also available on binding pocket entries (binding pockets can only be created in *CLC Drug Discovery Workbench*).
- Hydrogen Bonded Atoms. Creates at atom group that contains residues (for the protein and nucleic acid categories) and molecules (for the other categories) that have hydrogen bonds to the selected entries. Only atoms from currently visible Project Tree entries are considered.

If a Binding Site Setup is present in the Project Tree (A Binding Site Setup can only be created using *CLC Drug Discovery Workbench*), and entries from the Ligands or Docking results categories are selected, two extra options are available under the header **Create Atom Group (Binding Site)**. For these options, atom groups are created considering all molecules included in the Binding Site Setup, and thus not taking into account which Project Tree entries are currently visible.

Zoom to fit

(⇠⇢)

The "Zoom to fit" button can be used to automatically move a region of interest into the center of the screen. This can be done by selecting a molecule or category of interest in the Project Tree view followed by a click on the "Zoom to fit" button (⇠⇢) at the bottom of the Project Tree view (figure 10.8). Double-clicking an entry in the Project Tree will have the same effect.

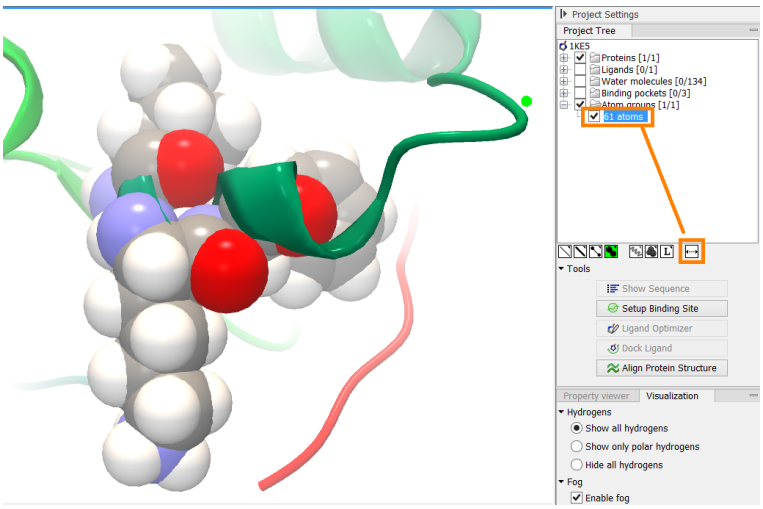

Figure 10.8: *The "Fit to screen" button can be used to bring a particular molecule or category of molecules in focus.*

10.3.2 Project settings

A number of general settings can be adjusted from the **Side Panel**. Personal settings as well as molecule visualizations can be saved by clicking in the lower right corner of the **Side Panel** ( ). This is described in detail in section 4.5.

Project Tree Tools

Just below the Project Tree, the following tools are available

- **Show Sequence** Select molecules which have sequences associated (Protein, DNA, RNA) in the Project Tree, and click this button. Then, a split-view will appear with a sequence list editor for each of the sequence data types (Protein, DNA, RNA). This is described in section 10.5.1.

Property viewer

The Property viewer, found in the Side Panel, lists detailed information about the atoms that the mouse hovers over. For all atoms the following information is listed:

- **Molecule** The name of the molecule the atom is part of.
- **Residue** For proteins and nucleic acids, the name and number of the residue the atom belongs to is listed, and the chain name is displayed in parentheses.
- **Name** The particular atom name, if given in input, with the element type (Carbon, Nitrogen, Oxygen...) displayed in parentheses.
- **Hybridization** The atom hybridization assigned to the atom.
- **Charge** The atomic charge as given in the input file. If charges are not given in the input file, some charged chemical groups are automatically recognized and a charge assigned.

For atoms in molecules imported from a PDB file, extra information is given:

- **Temperature** Here is listed the b-factor assigned to the atom in the PDB file. The b-factor is a measure of uncertainty or disorder in the atom position; the higher the number, the higher the disorder.
- **Occupancy** For each atom in a PDB file, the occupancy is given. It is typically 1, but if atoms are modeled in the PDB file, with no foundation in the raw data, the occupancy is 0. If a residue or molecule has been resolved in multiple positions, the occupancy is between 0 and 1.

If an atom is selected, the Property view will be frozen with the details of the selected atom shown. If then a second atom is selected (by holding down Ctrl while clicking), the distance between the two selected atoms is shown. If a third atom is selected, the angle for the second atom selected is shown. If a fourth atom is selected, the dihedral angle measured as the angle between the planes formed by the three first and three last selected atoms is given.

If a molecule is selected in the Project Tree, the Property view shows information about this molecule. Two measures are always shown:

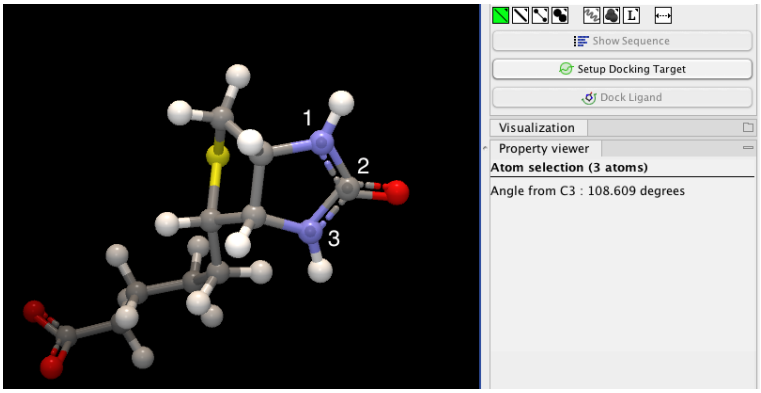

Figure 10.9: *Selecting two, three, or four atoms will display the distance, angle, or dihedral angle, respectively.*

- **Atoms** Number of atoms in the molecule.
- **Weight** The weight of the molecule in Daltons.

Visualization settings

Under "Visualization" five options exist:

- **Hydrogens** Hydrogen atoms can be shown (Show all hydrogens), hidden (Hide all hydrogens) or partially shown (Show only polar hydrogens).
- **Fog** "Fog" is added to give a sense of depth in the view. The strength of the fog can be adjusted or it can be disabled.
- **Clipping plane** This option makes it possible to add an imaginary plane at a specified distance along the camera's line of sight. Only objects behind this plane will be drawn. It is possible to clip only surfaces, or to clip surfaces together with proteins and nucleic acids. Small molecules, like ligands and water molecules, are never clipped.
- **3D projection** The view is opened up towards the viewer, with a "Perspective" 3D projection. The field of view of the perspective can be adjusted, or the perspective can be disabled by selecting an orthographic 3D projection.
- **Coloring** The background color can be selected from a color palette by clicking on the colored box.

10.4 Snapshots of the molecule visualization

To save the current view as a picture, right-click in the **View Area** and select "File" and "Export Graphics". Another way to save an image is by pressing the "Graphics" button in the Workbench toolbar ( ). Next, select the location where you wish to save the image, select file format (PNG, JPEG, or TIFF), and provide a name, if you wish to use another name than the default name.

You can also save the current view directly on data with a custom name, so that it can later be applied (see section 4.5).

10.5 Tools for linking sequence and structure

The *CLC Sequence Viewer* has functionality that allows you to link a protein sequence to a protein structure. Selections made on the sequence will show up on the structure. This allows you to explore a protein sequence in a 3D structure context.

10.5.1 Show sequence associated with molecule

From the Side Panel, sequences associated with the molecules in the Molecule Project can be opened as separate objects by selecting protein or nucleic acid entries in the Project Tree and clicking the button labeled "Show Sequence" (figure 10.10). This will generate a Sequence or Sequence List for each selected sequence type (protein, DNA, RNA). The sequences can be used to select atoms in the Molecular Project as described in section 10.3.1. The sequences can also be used as input for sequence analysis tools or be saved as independent objects.

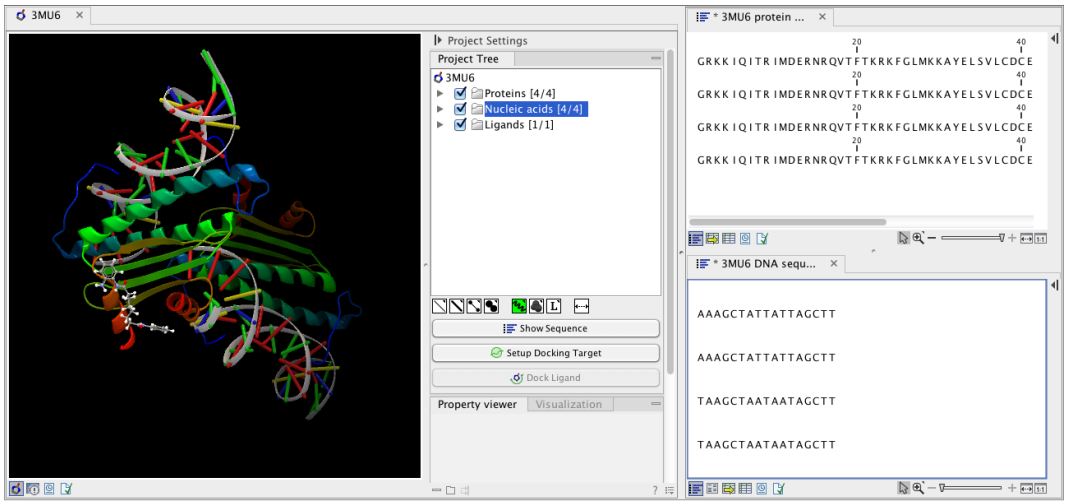

Figure 10.10: *Protein chain sequences and DNA sequences are shown in separate views.*

Chapter 11

Data download

Contents

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CLC Sequence Viewer allows you to search the for sequences on the Internet. You must be online when initiating and performing searches in NCBI.

11.1 GenBank search

This section describes searches for sequences in GenBank - the **NCBI Entrez** database. The NCBI search view is opened in this way (figure 11.1):

Download | Search for Sequences at NCBI ( )

or **Ctrl + B (⌘ + B on Mac)**

This opens the following view:

11.1.1 GenBank search options

Conducting a search in the **NCBI Database** from *CLC Sequence Viewer* corresponds to conducting the search on NCBI's website. When conducting the search from *CLC Sequence Viewer*, the results are available and ready to work with straight away.

You can choose whether you want to search for nucleotide sequences or protein sequences.

As default, *CLC Sequence Viewer* offers one text field where the search parameters can be entered. Click **Add search parameters** to add more parameters to your search.
Note! The search is a "and" search, meaning that when adding search parameters to your search, you search for both (or all) text strings rather than "any" of the text strings.

You can append a wildcard character by checking the checkbox at the bottom. This means that you only have to enter the first part of the search text, e.g. searching for "genom" will find both

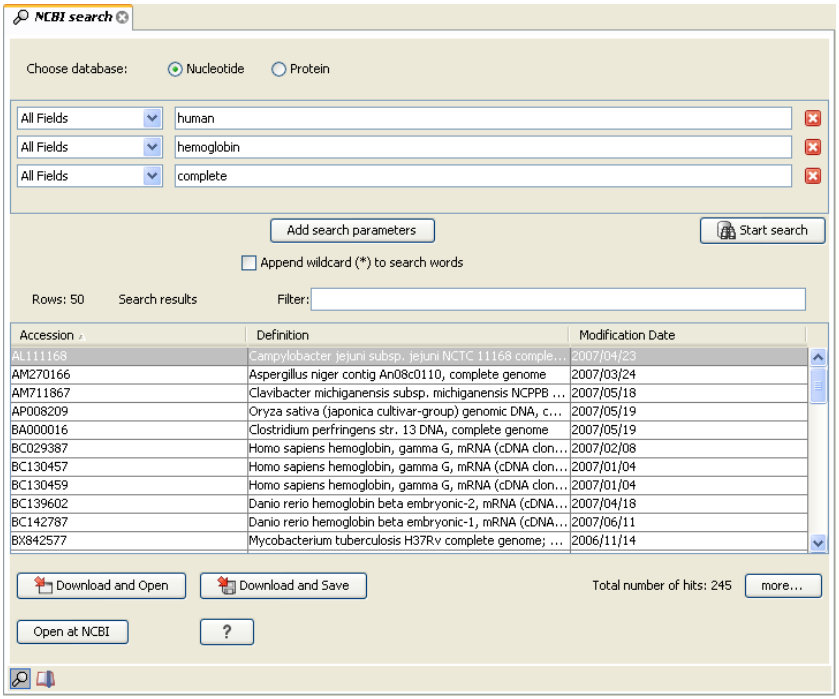
NCBI search
Choose database:
Nucleotide
Protein
All Fields
human
All Fields
hemoglobin
All Fields
complete
Add search parameters
Start search
Append wildcard (*) to search words
Rows: 50
Search results
Filter:
Accession
Definition
Modification Date
AL111168 Campylobacter jejuni subsp. jejuni NCTC 11168 comple... 2007/04/23
AM270166 Aspergillus niger contig An08c0110, complete genome 2007/03/24
AM711867 Clavibacter michiganensis subsp. michiganensis NCPPB ... 2007/05/18
AP008209 Oryza sativa (japonica cultivar-group) genomic DNA, c... 2007/05/19
BA000016 Clostridium perfringens str. 13 DNA, complete genome 2007/05/19
BC029387 Homo sapiens hemoglobin, gamma G, mRNA (cDNA clon... 2007/02/08
BC130457 Homo sapiens hemoglobin, gamma G, mRNA (cDNA clon... 2007/01/04
BC130459 Homo sapiens hemoglobin, gamma G, mRNA (cDNA clon... 2007/01/04
BC139602 Danio rerio hemoglobin beta embryonic-2, mRNA (cDNA... 2007/04/18
BC142787 Danio rerio hemoglobin beta embryonic-1, mRNA (cDNA... 2007/06/11
BX842577 Mycobacterium tuberculosis H37Rv complete genome; ... 2006/11/14
Download and Open
Download and Save
Total number of hits: 245
more...
Open at NCBI
?

Figure 11.1: *The GenBank search view.*

"genomic" and "genome".

The following parameters can be added to the search:

- **All fields**. Text, searches in all parameters in the NCBI database at the same time.
- **Organism**. Text.
- **Description**. Text.
- **Modified Since**. Between 30 days and 10 years.
- **Gene Location**. Genomic DNA/RNA, Mitochondrion, or Chloroplast.
- **Molecule**. Genomic DNA/RNA, mRNA or rRNA.
- **Sequence Length**. Number for maximum or minimum length of the sequence.
- **Gene Name**. Text.

The search parameters are the most recently used. The **All fields** allows searches in all parameters in the NCBI database at the same time. **All fields** also provide an opportunity to restrict a search to parameters which are not listed in the dialog. E.g. writing `gene[Feature key] AND mouse` in **All fields** generates hits in the GenBank database which contains one or more genes and where 'mouse' appears somewhere in GenBank file. You can also write e.g. `CD9 NOT homo sapiens` in **All fields**.

Note! The 'Feature Key' option is only available in GenBank when searching for nucleotide sequences. For more information about how to use this syntax, see `http://www.ncbi.nlm.nih.gov/books/NBK3837/`

When you are satisfied with the parameters you have entered, click **Start search**.

Note! When conducting a search, no files are downloaded. Instead, the program produces a list of links to the files in the NCBI database. This ensures a much faster search.

11.1.2 Handling of GenBank search results

The search result is presented as a list of links to the files in the NCBI database. The **View** displays 50 hits at a time. This can be changed in the **Preferences** (see chapter 4). More hits can be displayed by clicking the **More...** button at the bottom right of the **View**.

Each sequence hit is represented by text in three columns:

- Accession.
- Description.
- Modification date.
- Length.

It is possible to exclude one or more of these columns by adjust the View preferences for the database search view. Furthermore, your changes in the View preferences can be saved. See section 4.5.

Several sequences can be selected, and by clicking the buttons in the bottom of the search view, you can do the following:

- Download and open, doesn't save the sequence.
- Download and save, lets you choose location for saving sequence.
- Open at NCBI, searches the sequence at NCBI's web page.

Double-clicking a hit will download and open the sequence. The hits can also be copied into the **View Area** or the **Navigation Area** from the search results by drag and drop, copy/paste or by using the right-click menu as described below.

Drag and drop from GenBank search results

The sequences from the search results can be opened by dragging them into a position in the **View Area**.

Note! A sequence is not saved until the **View** displaying the sequence is closed. When that happens, a dialog opens: Save changes of sequence x? (Yes or No).

The sequence can also be saved by dragging it into the **Navigation Area**. It is possible to select more sequences and drag all of them into the **Navigation Area** at the same time.

Download GenBank search results using right-click menu

You may also select one or more sequences from the list and download using the right-click menu (see figure 11.2). Choosing **Download and Save** lets you select a folder where the sequences are saved when they are downloaded. Choosing **Download and Open** opens a new view for each of the selected sequences.

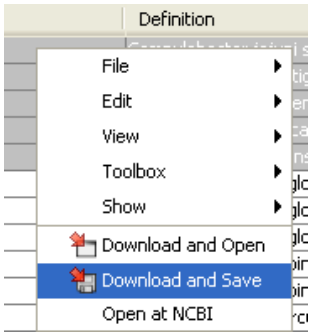

Figure 11.2: *By right-clicking a search result, it is possible to choose how to handle the relevant sequence.*

Copy/paste from GenBank search results

When using copy/paste to bring the search results into the **Navigation Area**, the actual files are downloaded from GenBank.

To copy/paste files into the **Navigation Area**:

> **select one or more of the search results | Ctrl + C (⌘ + C on Mac) | select a folder in the Navigation Area | Ctrl + V**

Note! Search results are downloaded before they are saved. Downloading and saving several files may take some time. However, since the process runs in the background (displayed in the **Status bar**) it is possible to continue other tasks in the program. Like the search process, the download process can be stopped. This is done in the **Toolbox** in the **Processes** tab.

11.1.3 Save GenBank search parameters

The search view can be saved either using dragging the search tab and and dropping it in the **Navigation Area** or by clicking **Save** ( ). When saving the search, only the parameters are saved - not the results of the search. This is useful if you have a special search that you perform from time to time.

Even if you don't save the search, the next time you open the search view, it will remember the parameters from the last time you did a search.

Chapter 12

General sequence analyses

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CLC Sequence Viewer offers different kinds of sequence analyses, which apply to both protein and DNA.

12.1 Extract sequences

This tool allows the extraction of sequences from other types of data in the Workbench, such as sequence lists or alignments. The data types you can extract sequences from are:

- Alignments ( )
- BLAST result ( )
- BLAST overview tables ( )
- sequence lists ( )
- Contigs and read mappings ( )
- Read mapping tables ( )
- Read mapping tracks ( )
- RNA-Seq mapping results ( )

Note! When the Extract Sequences tool is run via the Workbench toolbox on an entire file of one of the above types, **all** sequences are extracted from the data used as input. If only a **subset** of the sequences is desired, for example, the reads from just a small area of a mapping, or the

sequences for only a few blast results, then a data set containing just this subsection or subset should be created and the Extract Sequences tool should be run on that.

For extracting a subset of a mapping, please see section **??** that describes the function "Extract from Selection" that also can be selected from the right click menu (see figure 12.1).

For extracting a subset of a sequence list, you can highlight the sequences of interest in the table view of the sequence list, right click on the selection and launch the Extract Sequences tool.

The Extract Sequences tool can be launched via the Toolbox menu, by going to:

Toolbox | **General Sequence Analysis** ( )| **Extract Sequences** ( )

Alternatively, on all the data types listed above except sequence lists, the option to run this tool appears by right clicking in the relevant area; a row in a table or in the read area of mapping data. An example is shown in figure 12.1.

Please note that for mappings, only the read sequences are extracted. Reference and consensus sequences are not extracted using this tool. Similarly, when extracting sequences from BLAST results, the sequence hits are extracted, not the original query sequence or a consensus sequence.

"Note also, that paired reads will be extracted in accordance with the read group settings, which is specified during the original import of the reads. If the orientation has since been changed (e.g. using the Element Info tab for the sequence list) the read group information will be modified and reads will be extracted as specified by the modified read group. The default read group orientation is forward-reverse."

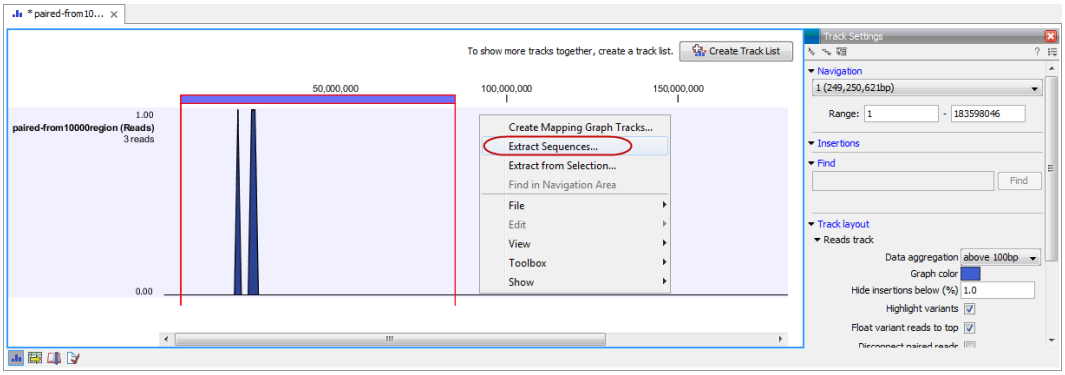


Figure 12.1: *Right click somewhere in the reads track area and select "Extract Sequences".*

The dialog allows you to select the **Destination**. Here you can choose whether the extracted sequences should be extracted as single sequences or placed in a new sequence list. For most data types, it will make most sense to choose to extract the sequences into a sequence list. The exception to this is when working with a sequence list, where choosing to extract to a sequence list would create a copy of the same sequence list. In this case, the other option would generally be chosen. This would then result in the generation of individual sequence objects for each sequence in the sequence list.

Below these options, in the dialog, you can see the number of sequences that will be extracted.

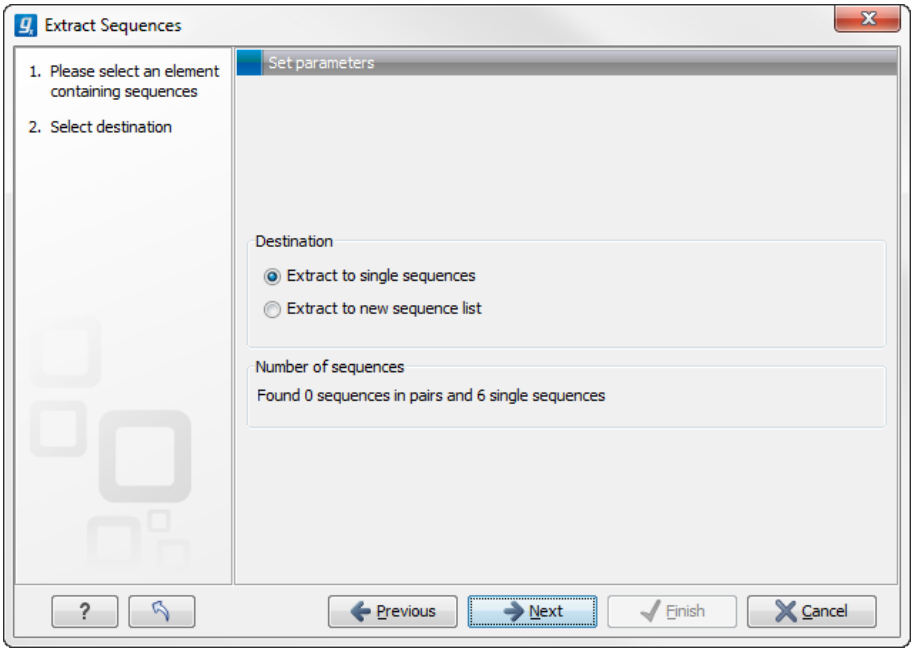


Figure 12.2: *Choosing whether the extracted sequences should be placed in a new list or as single sequences.*

12.2 Shuffle sequence

In some cases, it is beneficial to shuffle a sequence. This is an option in the **Toolbox** menu under **General Sequence Analyses**. It is normally used for statistical analyses, e.g. when comparing an alignment score with the distribution of scores of shuffled sequences.

Shuffling a sequence removes all annotations that relate to the residues. To launch the tool, go to:

Toolbox | **General Sequence Analysis** ( )| **Shuffle Sequence** ( )

This opens the dialog displayed in figure 12.3:

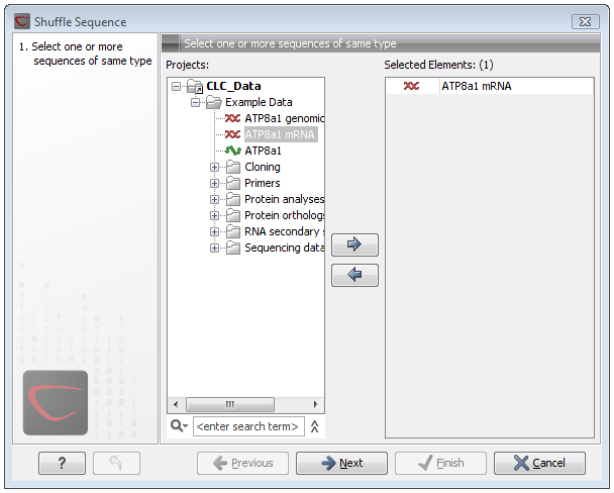


Figure 12.3: *Choosing sequence for shuffling.*

If a sequence was selected before choosing the Toolbox action, this sequence is now listed in

the **Selected Elements** window of the dialog. Use the arrows to add or remove sequences or sequence lists, from the selected elements.

Click **Next** to determine how the shuffling should be performed.

In this step, shown in figure 12.4:

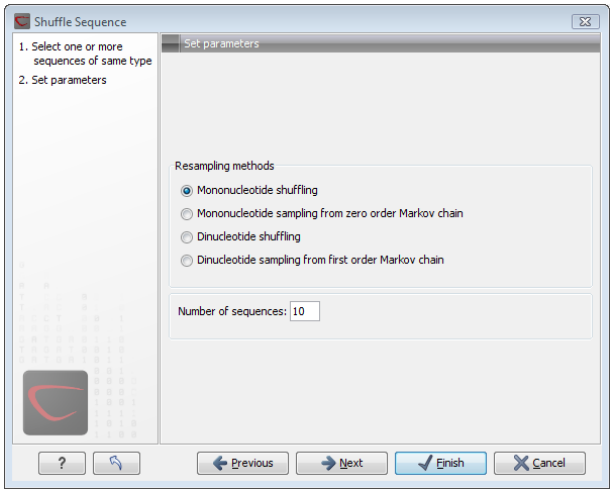


Figure 12.4: *Parameters for shuffling.*

For nucleotides, the following parameters can be set:

- **Mononucleotide shuffling.** Shuffle method generating a sequence of the exact same mononucleotide frequency
- **Dinucleotide shuffling.** Shuffle method generating a sequence of the exact same dinucleotide frequency
- **Mononucleotide sampling from zero order Markov chain.** Resampling method generating a sequence of the same expected mononucleotide frequency.
- **Dinucleotide sampling from first order Markov chain.** Resampling method generating a sequence of the same expected dinucleotide frequency.

For proteins, the following parameters can be set:

- **Single amino acid shuffling.** Shuffle method generating a sequence of the exact same amino acid frequency.
- **Single amino acid sampling from zero order Markov chain.** Resampling method generating a sequence of the same expected single amino acid frequency.
- **Dipeptide shuffling.** Shuffle method generating a sequence of the exact same dipeptide frequency.
- **Dipeptide sampling from first order Markov chain.** Resampling method generating a sequence of the same expected dipeptide frequency.

For further details of these algorithms, see [Clote et al., 2005]. In addition to the shuffle method, you can specify the number of randomized sequences to output.

Click **Next** if you wish to adjust how to handle the results (see section 8.1). If not, click **Finish**.

This will open a new view in the **View Area** displaying the shuffled sequence. The new sequence is not saved automatically. To save the sequence, drag it into the **Navigation Area** or press ctrl + S (⌘ + S on Mac) to activate a save dialog.

12.3 Sequence statistics

CLC Sequence Viewer can produce an output with many relevant statistics for protein sequences. Some of the statistics are also relevant to produce for DNA sequences. Therefore, this section deals with both types of statistics. The required steps for producing the statistics are the same.

To create a statistic for the sequence, do the following:

Toolbox | **General Sequence Analysis** ( )| **Create Sequence Statistics** ( )

This opens a dialog where you can alter your choice of sequences. If you had already selected sequences in the Navigation Area, these will be shown in the **Selected Elements** window. However you can remove these, or add others, by using the arrows to move sequences in or out of the **Selected Elements** window. You can also add sequence lists.

Note! You cannot create statistics for DNA and protein sequences at the same time; they must be run separately.

When the sequences are selected, click **Next**.

This opens the dialog displayed in figure 12.5.

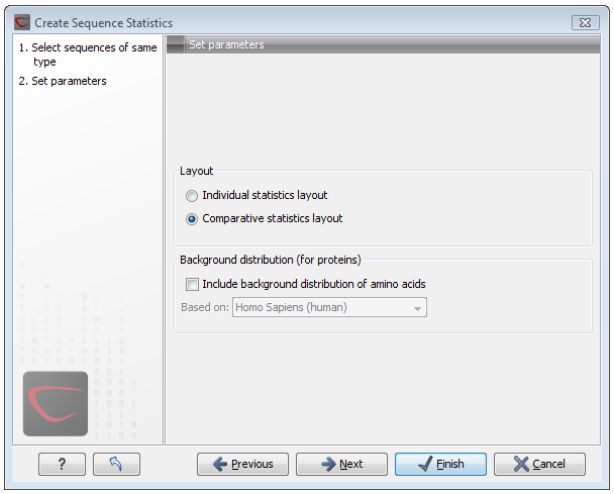


Figure 12.5: *Setting parameters for the sequence statistics.*

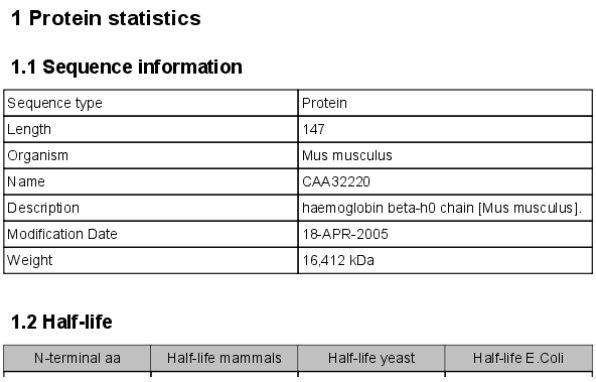
The dialog offers to adjust the following parameters:

- **Individual statistics layout.** If more sequences were selected in **Step 1**, this function generates separate statistics for each sequence.
- **Comparative statistics layout.** If more sequences were selected in **Step 1**, this function

generates statistics with comparisons between the sequences.

You can also choose to include Background distribution of amino acids. If this box is ticked, an extra column with amino acid distribution of the chosen species, is included in the table output. (The distributions are calculated from UniProt `www.uniprot.org` version 6.0, dated September 13 2005.)

Click **Next** if you wish to adjust how to handle the results (see section 8.1). If not, click **Finish**. An example of protein sequence statistics is shown in figure 12.6.



1 Protein statistics

1.1 Sequence information

Sequence type	Protein
Length	147
Organism	Mus musculus
Name	CAA32220
Description	haemoglobin beta-h0 chain [Mus musculus].
Modification Date	18-APR-2005
Weight	16,412 kDa

1.2 Half-life

N-terminal aa	Half-life mammals	Half-life yeast	Half-life E.Coli

Figure 12.6: *Example of protein sequence statistics.*

Nucleotide sequence statistics are generated using the same dialog as used for protein sequence statistics. However, the output of Nucleotide sequence statistics is less extensive than that of the protein sequence statistics.

Note! The headings of the tables change depending on whether you calculate 'individual' or 'comparative' sequence statistics.

The output of comparative protein sequence statistics include:

- Sequence information:
  - Sequence type
  - Length
  - Organism
  - Name
  - Description
  - Modification Date
  - Weight. This is calculated like this: $sum_{unitsinsequence}(weight(unit)) - links * weight(H2O)$ where `links` is the sequence length minus one and `units` are amino acids. The atomic composition is defined the same way.
  - Isoelectric point
  - Aliphatic index

- Sequence Information:
  - Sequence type

  - Length
  - Organism
  - Name
  - Description
  - Modification Date
  - Weight
  - Isoelectric point
  - Aliphatic index
- Amino acid distribution
- Annotation table

The output of nucleotide sequence statistics include:

- General statistics:
  - Sequence type
  - Length
  - Organism
  - Name
  - Description
  - Modification Date
  - Weight (calculated as single-stranded DNA)
- Nucleotide distribution table
- Annotation table

If nucleotide sequences are used as input, and these are annotated with CDS, a section on Codon statistics for Coding Regions is included.

12.3.1 Bioinformatics explained: Protein statistics

Every protein holds specific and individual features which are unique to that particular protein. Features such as isoelectric point or amino acid composition can reveal important information of a novel protein. Many of the features described below are calculated in a simple way.

Molecular weight

The molecular weight is the mass of a protein or molecule. The molecular weight is simply calculated as the sum of the atomic mass of all the atoms in the molecule.

The weight of a protein is usually represented in Daltons (Da).

A calculation of the molecular weight of a protein does not usually include additional posttranslational modifications. For native and unknown proteins it tends to be difficult to assess whether posttranslational modifications such as glycosylations are present on the protein, making a calculation based solely on the amino acid sequence inaccurate. The molecular weight can be determined very accurately by mass-spectrometry in a laboratory.

Isoelectric point

The isoelectric point (pI) of a protein is the pH where the proteins has no net charge. The pI is calculated from the pKa values for 20 different amino acids. At a pH below the pI, the protein carries a positive charge, whereas if the pH is above pI the proteins carry a negative charge. In other words, pI is high for basic proteins and low for acidic proteins. This information can be used in the laboratory when running electrophoretic gels. Here the proteins can be separated, based on their isoelectric point.

Aliphatic index

The aliphatic index of a protein is a measure of the relative volume occupied by aliphatic side chain of the following amino acids: alanine, valine, leucine and isoleucine. An increase in the aliphatic index increases the thermostability of globular proteins. The index is calculated by the following formula.

$$Aliphaticindex = X(Ala) + a * X(Val) + b * X(Leu) + b * (X)Ile$$

X(Ala), *X(Val)*, *X(Ile)* and *X(Leu)* are the amino acid compositional fractions. The constants a and b are the relative volume of valine (a=2.9) and leucine/isoleucine (b=3.9) side chains compared to the side chain of alanine [Ikai, 1980].

Estimated half-life

The half life of a protein is the time it takes for the protein pool of that particular protein to be reduced to the half. The half life of proteins is highly dependent on the presence of the N-terminal amino acid, thus overall protein stability [Bachmair et al., 1986, Gonda et al., 1989, Tobias et al., 1991]. The importance of the N-terminal residues is generally known as the 'N-end rule'. The N-end rule and consequently the N-terminal amino acid, simply determines the half-life of proteins. The estimated half-life of proteins have been investigated in mammals, yeast and *E. coli* (see Table 12.1). If leucine is found N-terminally in mammalian proteins the estimated half-life is 5.5 hours.

Extinction coefficient

This measure indicates how much light is absorbed by a protein at a particular wavelength. The extinction coefficient is measured by UV spectrophotometry, but can also be calculated. The amino acid composition is important when calculating the extinction coefficient. The extinction coefficient is calculated from the absorbance of cysteine, tyrosine and tryptophan using the following equation:

$$Ext(Protein) = count(Cystine) * Ext(Cystine) + count(Tyr) * Ext(Tyr) + count(Trp) * Ext(Trp)$$

where Ext is the extinction coefficient of amino acid in question. At 280nm the extinction coefficients are: Cys=120, Tyr=1280 and Trp=5690.

This equation is only valid under the following conditions:

- pH 6.5
- 6.0 M guanidium hydrochloride

Amino acid	Mammalian	Yeast	E. coli
Ala (A)	4.4 hour	>20 hours	>10 hours
Cys (C)	1.2 hours	>20 hours	>10 hours
Asp (D)	1.1 hours	3 min	>10 hours
Glu (E)	1 hour	30 min	>10 hours
Phe (F)	1.1 hours	3 min	2 min
Gly (G)	30 hours	>20 hours	>10 hours
His (H)	3.5 hours	10 min	>10 hours
Ile (I)	20 hours	30 min	>10 hours
Lys (K)	1.3 hours	3 min	2 min
Leu (L)	5.5 hours	3 min	2 min
Met (M)	30 hours	>20 hours	>10 hours
Asn (N)	1.4 hours	3 min	>10 hours
Pro (P)	>20 hours	>20 hours	?
Gln (Q)	0.8 hour	10 min	>10 hours
Arg (R)	1 hour	2 min	2 min
Ser (S)	1.9 hours	>20 hours	>10 hours
Thr (T)	7.2 hours	>20 hours	>10 hours
Val (V)	100 hours	>20 hours	>10 hours
Trp (W)	2.8 hours	3 min	2 min
Tyr (Y)	2.8 hours	10 min	2 min

Table 12.1: **Estimated half life**. Half life of proteins where the N-terminal residue is listed in the first column and the half-life in the subsequent columns for mammals, yeast and *E. coli*.

- 0.02 M phosphate buffer

The extinction coefficient values of the three important amino acids at different wavelengths are found in [Gill and von Hippel, 1989].

Knowing the extinction coefficient, the absorbance (optical density) can be calculated using the following formula:

$$Absorbance(Protein) = \frac{Ext(Protein)}{Molecular\ weight}$$

Two values are reported. The first value is computed assuming that all cysteine residues appear as half cystines, meaning they form di-sulfide bridges to other cysteines. The second number assumes that no di-sulfide bonds are formed.

Atomic composition

Amino acids are indeed very simple compounds. All 20 amino acids consist of combinations of only five different atoms. The atoms which can be found in these simple structures are: Carbon, Nitrogen, Hydrogen, Sulfur, Oxygen. The atomic composition of a protein can for example be used to calculate the precise molecular weight of the entire protein.

Total number of negatively charged residues (Asp+Glu)

At neutral pH, the fraction of negatively charged residues provides information about the location of the protein. Intracellular proteins tend to have a higher fraction of negatively charged residues than extracellular proteins.

Total number of positively charged residues (Arg+Lys)

At neutral pH, nuclear proteins have a high relative percentage of positively charged amino acids. Nuclear proteins often bind to the negatively charged DNA, which may regulate gene expression or help to fold the DNA. Nuclear proteins often have a low percentage of aromatic residues [Andrade et al., 1998].

Amino acid distribution

Amino acids are the basic components of proteins. The amino acid distribution in a protein is simply the percentage of the different amino acids represented in a particular protein of interest. Amino acid composition is generally conserved through family-classes in different organisms which can be useful when studying a particular protein or enzymes across species borders. Another interesting observation is that amino acid composition variate slightly between proteins from different subcellular localizations. This fact has been used in several computational methods, used for prediction of subcellular localization.

Annotation table

This table provides an overview of all the different annotations associated with the sequence and their incidence.

Dipeptide distribution

This measure is simply a count, or frequency, of all the observed adjacent pairs of amino acids (dipeptides) found in the protein. It is only possible to report neighboring amino acids. Knowledge on dipeptide composition have previously been used for prediction of subcellular localization.

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12.4 Join sequences

CLC Sequence Viewer can join several nucleotide or protein sequences into one sequence. This feature can for example be used to construct "supergenes" for phylogenetic inference by joining several disjoint genes into one. Note, that when sequences are joined, all their annotations are carried over to the new spliced sequence.

Two (or more) sequences can be joined by:

Toolbox | **General Sequence Analyses** | **Join sequences** ( )

This opens the dialog shown in figure 12.7.

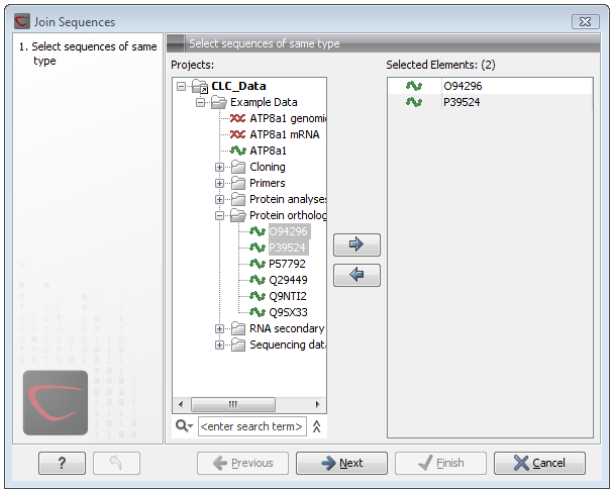

Figure 12.7: *Selecting two sequences to be joined.*

If you have selected some sequences before choosing the Toolbox action, they are now listed in the **Selected Elements** window of the dialog. Use the arrows to add or remove sequences from the selected elements. Click **Next** opens the dialog shown in figure 12.8.

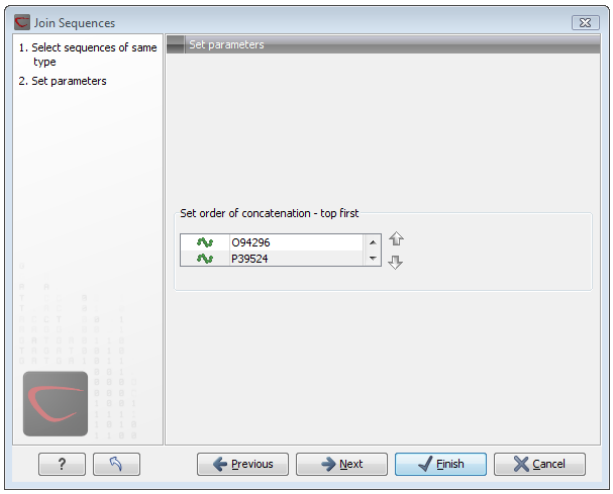

Figure 12.8: *Setting the order in which sequences are joined.*

In step 2 you can change the order in which the sequences will be joined. Select a sequence and use the arrows to move the selected sequence up or down.

Click **Next** if you wish to adjust how to handle the results (see section 8.1). If not, click **Finish**.

The result is shown in figure 12.9.

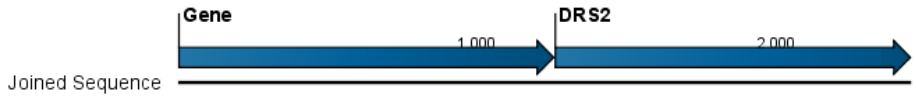

Figure 12.9: *The result of joining sequences is a new sequence containing the annotations of the joined sequences (they each had a HBB annotation).*

Chapter 13

Nucleotide analyses

Contents

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CLC Sequence Viewer offers different kinds of sequence analyses, which only apply to DNA and RNA.

13.1 Convert DNA to RNA

CLC Sequence Viewer lets you convert a DNA sequence into RNA, substituting the T residues (Thymine) for U residues (Urasil):

Toolbox | **Nucleotide Analysis (** **)**| **Convert DNA to RNA** **(** **)**

This opens the dialog displayed in figure 13.1:

If a sequence was selected before choosing the Toolbox action, this sequence is now listed in the **Selected Elements** window of the dialog. Use the arrows to add or remove sequences or sequence lists from the selected elements.

Click **Next** if you wish to adjust how to handle the results (see section 8.1). If not, click **Finish**.

Note! You can select multiple DNA sequences and sequence lists at a time. If the sequence list contains RNA sequences as well, they will not be converted.

13.2 Convert RNA to DNA

CLC Sequence Viewer lets you convert an RNA sequence into DNA, substituting the U residues (Urasil) for T residues (Thymine):

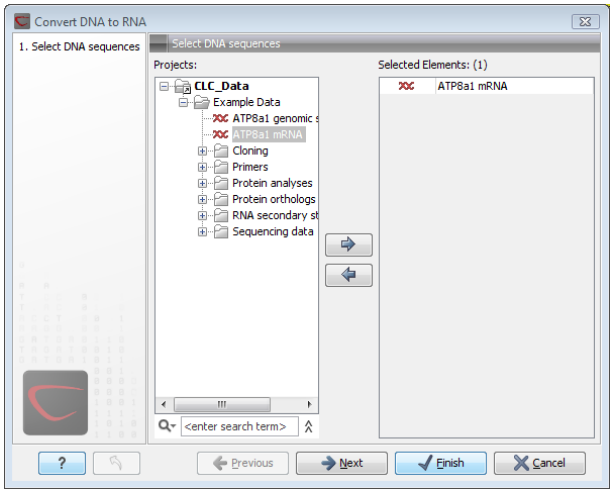

Figure 13.1: *Translating DNA to RNA.*

Toolbox | **Nucleotide Analysis** ( )| **Convert RNA to DNA** ( )

This opens the dialog displayed in figure 13.2:

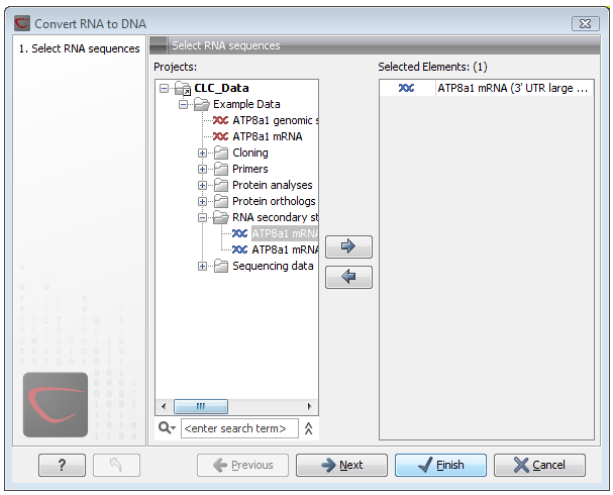

Figure 13.2: *Translating RNA to DNA.*

If a sequence was selected before choosing the Toolbox action, this sequence is now listed in the **Selected Elements** window of the dialog. Use the arrows to add or remove sequences or sequence lists from the selected elements.

Click **Next** if you wish to adjust how to handle the results (see section 8.1). If not, click **Finish**.

This will open a new view in the **View Area** displaying the new DNA sequence. The new sequence is not saved automatically. To save the sequence, drag it into the **Navigation Area** or press Ctrl + S (⌘ + S on Mac) to activate a save dialog.

Note! You can select multiple RNA sequences and sequence lists at a time. If the sequence list contains DNA sequences as well, they will not be converted.

13.3 Reverse complements of sequences

CLC Sequence Viewer is able to create the reverse complement of a nucleotide sequence. By doing that, a new sequence is created which also has all the annotations reversed since they now occupy the opposite strand of their previous location.

To quickly obtain the reverse complement of a sequence or part of a sequence, you may select a region on the negative strand and open it in a new view:

right-click a selection on the negative strand | **Open selection in New View (** **)**

By doing that, the sequence will be reversed. This is only possible when the double stranded view option is enabled. It is possible to copy the selection and paste it in a word processing program or an e-mail. To obtain a reverse complement of an entire sequence:

Toolbox | **Nucleotide Analysis (** **)**| **Reverse Complement Sequence (** **)**

This opens the dialog displayed in figure 13.3:

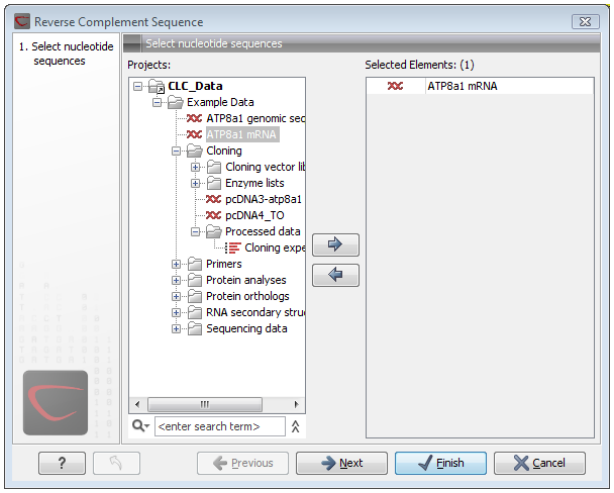

Figure 13.3: *Creating a reverse complement sequence.*

If a sequence was selected before choosing the Toolbox action, the sequence is now listed in the **Selected Elements** window of the dialog. Use the arrows to add or remove sequences or sequence lists from the selected elements.

Click **Next** if you wish to adjust how to handle the results (see section 8.1). If not, click **Finish**.

This will open a new view in the **View Area** displaying the reverse complement of the selected sequence. The new sequence is not saved automatically. To save the sequence, drag it into the **Navigation Area** or press Ctrl + S (⌘ + S on Mac) to activate a save dialog.

13.4 Reverse sequence

CLC Sequence Viewer is able to create the reverse of a nucleotide sequence.

Note! This is not the same as a reverse complement. If you wish to create the reverse complement, please refer to section 13.3.

To run the tool, go to:

Toolbox | **Nucleotide Analysis** ( )| **Reverse Sequence** ( )

This opens the dialog displayed in figure 13.4:

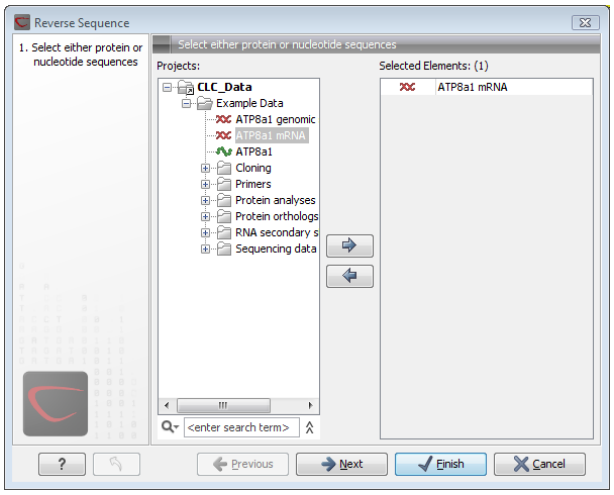

Figure 13.4: *Reversing a sequence.*

If a sequence was selected before choosing the Toolbox action, the sequence is now listed in the **Selected Elements** window of the dialog. Use the arrows to add or remove sequences or sequence lists from the selected elements.

Click **Next** if you wish to adjust how to handle the results (see section 8.1). If not, click **Finish**.

Note! This is not the same as a reverse complement. If you wish to create the reverse complement, please refer to section 13.3.

13.5 Translation of DNA or RNA to protein

In *CLC Sequence Viewer* you can translate a nucleotide sequence into a protein sequence using the **Toolbox** tools. Usually, you use the +1 reading frame which means that the translation starts from the first nucleotide. Stop codons result in an asterisk being inserted in the protein sequence at the corresponding position. It is possible to translate in any combination of the six reading frames in one analysis. To translate, go to:

Toolbox | **Nucleotide Analysis** ( )| **Translate to Protein** ( )

This opens the dialog displayed in figure 13.5:

If a sequence was selected before choosing the Toolbox action, the sequence is now listed in the **Selected Elements** window of the dialog. Use the arrows to add or remove sequences or sequence lists from the selected elements.

Clicking **Next** generates the dialog seen in figure 13.6:

Here you have the following options:

Reading frames If you wish to translate the whole sequence, you must specify the reading frame for the translation. If you select e.g. two reading frames, two protein sequences are generated.

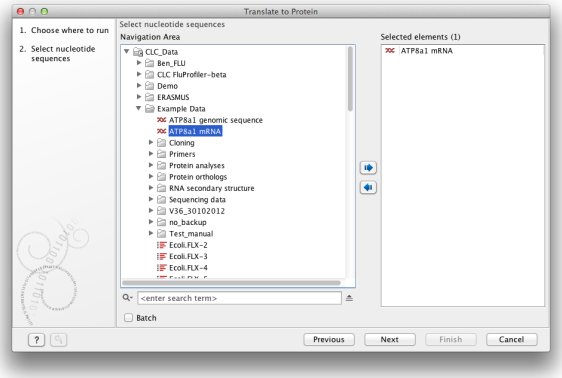

Figure 13.5: *Choosing sequences for translation.*

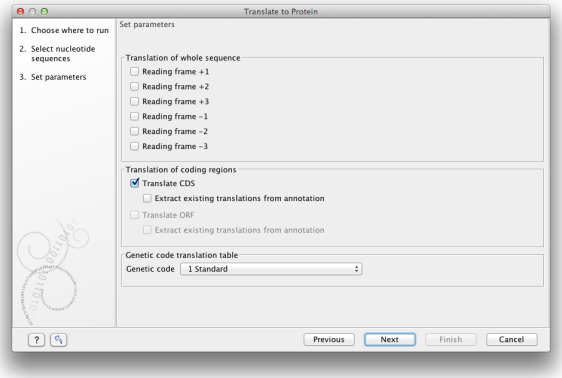

Figure 13.6: *Choosing translation of CDS's using standard translation table.*

Translate CDS You can choose to translate regions marked by and CDS or ORF annotation. This will generate a protein sequence for each CDS or ORF annotation on the sequence. The "Extract existing translations from annotation" allows to list the amino acid CDS sequence shown in the tool tip annotation (e.g. interstate from NCBI download) and does therefore not represent a translation of the actual nt sequence.

Genetic code translation table Lets you specify the genetic code for the translation. The translation tables are occasionally updated from NCBI. The tables are not available in this printable version of the user manual. Instead, the tables are included in the **Help**-menu in the **Menu Bar** (in the appendix).

Click **Next** if you wish to adjust how to handle the results (see section 8.1). If not, click **Finish**. The newly created protein is shown, but is not saved automatically.

To save a protein sequence, drag it into the **Navigation Area** or press Ctrl + S (⌘ + S on Mac) to activate a save dialog.

The name for a coding region translation consists of the name of the input sequence followed by the annotation type and finally the annotation name.

13.6 Find open reading frames

The *CLC Sequence Viewer* **Find Open Reading Frames** function can be used to find all open reading frames (ORF) in a sequence, or, by choosing particular start codons to use, it can be used as a rudimentary gene finder. ORFs identified will be shown as annotations on the sequence. You have the option of choosing a translation table, the start codons to use, minimum ORF length as well as a few other parameters. These choices are explained in this section.

To find open reading frames:

Toolbox | **Nucleotide Analysis** ( )| **Find Open Reading Frames** ( )

This opens the dialog displayed in figure 13.7:

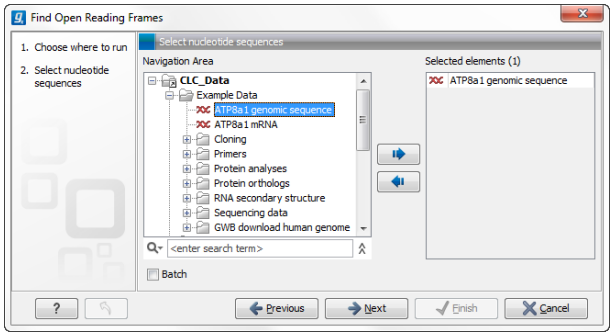

Figure 13.7: *Create Reading Frame dialog.*

If a sequence was selected before choosing the Toolbox action, the sequence is now listed in the **Selected Elements** window of the dialog. Use the arrows to add or remove sequences or sequence lists from the selected elements.

The **Find Open Reading Frames** tool simply looks for start and stop codons and reports any open reading frames that satisfy the parameters. If you want to adjust the parameters for finding open reading frames click **Next**.

13.6.1 Open reading frame parameters

This opens the dialog displayed in figure 13.8:

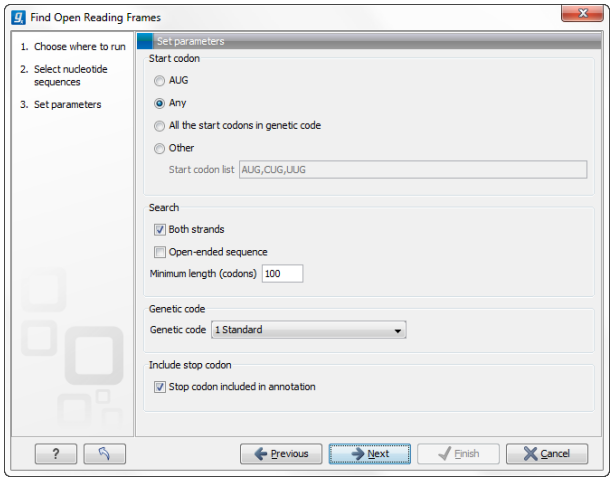

Figure 13.8: *Create Reading Frame dialog.*

The adjustable parameters for the search are:

- **Start codon**:
  - **AUG**. Most commonly used start codon.
  - **Any**. Find all open reading frames of specified length. Any combination of three bases that is not a stop-codon is interpreted as a start codon, and translated according to the specified genetic code.
  - **All start codons in genetic code**.
  - **Other**. Here you can specify a number of start codons separated by commas.
- **Both strands**. Finds reading frames on both strands.
- **Open-ended Sequence**. Allows the ORF to start or end outside the sequence. If the sequence studied is a part of a larger sequence, it may be advantageous to allow the ORF to start or end outside the sequence.
- **Genetic code translation table**.
- **Include stop codon in result** The ORFs will be shown as annotations which can include the stop codon if this option is checked. The translation tables are occasionally updated from NCBI. The tables are not available in this printable version of the user manual. Instead, the tables are included in the **Help**-menu in the **Menu Bar** (in the appendix).
- **Minimum Length**. Specifies the minimum length for the ORFs to be found. The length is specified as number of codons.

Using open reading frames for gene finding is a fairly simple approach which is likely to predict genes which are not real. Setting a relatively high minimum length of the ORFs will reduce the number of false positive predictions, but at the same time short genes may be missed (see figure 13.9).

Click **Next** if you wish to adjust how to handle the results (see section 8.1). If not, click **Finish**.

Finding open reading frames is often a good first step in annotating sequences such as cloning vectors or bacterial genomes. For eukaryotic genes, ORF determination may not always be very helpful since the intron/exon structure is not part of the algorithm.

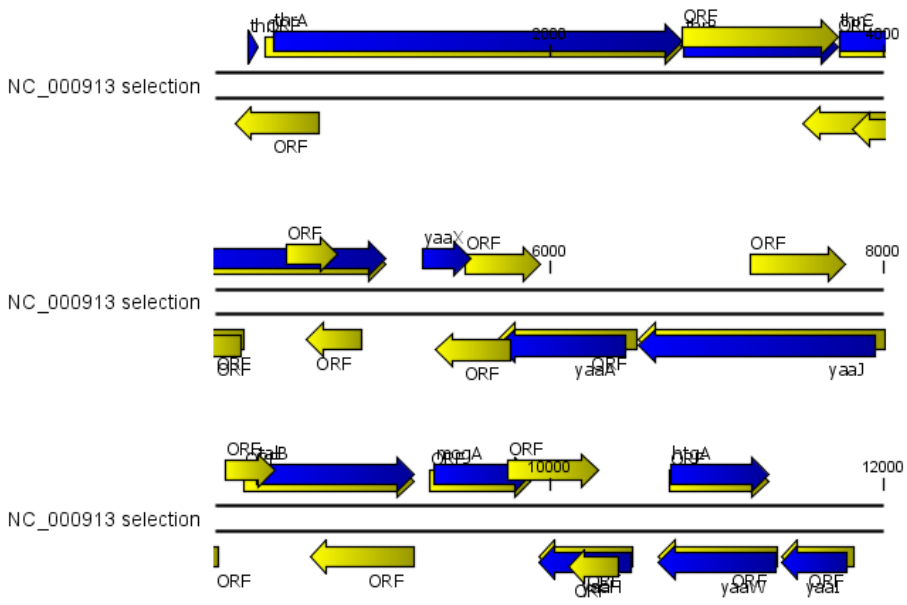

Figure 13.9: *The first 12,000 positions of the* E. coli *sequence NC_000913 downloaded from GenBank. The blue (dark) annotations are the genes while the yellow (brighter) annotations are the ORFs with a length of at least 100 amino acids. On the positive strand around position 11,000, a gene starts before the ORF. This is due to the use of the standard genetic code rather than the bacterial code. This particular gene starts with CTG, which is a start codon in bacteria. Two short genes are entirely missing, while a handful of open reading frames do not correspond to any of the annotated genes.*

Chapter 14

Restriction site analyses

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There are two ways of finding and showing restriction sites:

- In many cases, the dynamic restriction sites found in the **Side Panel** of sequence views will be useful, since it is a quick and easy way of showing restriction sites.
- In the **Toolbox** you will find the other way of doing restriction site analyses. This way provides more control of the analysis and gives you more output options, e.g. a table of restriction sites and you can perform the same restriction map analysis on several sequences in one step.

This chapter first describes the dynamic restriction sites, followed by "the toolbox way" (you can run more extensive analysis via the restriction analysis tools available via the toolbox). The final section in this chapter focuses on enzyme lists which represent an easy way of managing restriction enzymes.

14.1 Dynamic restriction sites

If you open a sequence, a sequence list etc, you will find the **Restriction Sites** group in the **Side Panel**.

As shown in figure 14.1 you can display restriction sites as colored triangles and lines on the sequence. The **Restriction sites** group in the side panel shows a list of enzymes, represented by different colors corresponding to the colors of the triangles on the sequence. By selecting or deselecting the enzymes in the list, you can specify which enzymes' restriction sites should be displayed.

Figure 14.1: *Showing restriction sites of ten restriction enzymes.*

The color of the restriction enzyme can be changed by clicking the colored box next to the enzyme's name. The name of the enzyme can also be shown next to the restriction site by selecting **Show name flags** above the list of restriction enzymes.

There is also an option to specify how the **Labels** shown be shown:

- **No labels**. This will just display the cut site with no information about the name of the enzyme. Placing the mouse button on the cut site will reveal this information as a tool tip.
- **Flag**. This will place a flag just above the sequence with the enzyme name (see an example in figure 14.2). Note that this option will make it hard to see when several cut sites are located close to each other. In the circular view, this option is replaced by the Radial option:
- **Radial**. This option is only available in the circular view. It will place the restriction site labels as close to the cut site as possible (see an example in figure 14.4).
- **Stacked**. This is similar to the flag option for linear sequence views, but it will stack the labels so that all enzymes are shown. For circular views, it will align all the labels on each side of the circle. This can be useful for clearly seeing the order of the cut sites when they are located closely together (see an example in figure 14.3).

Note that in a circular view, the **Stacked** and **Radial** options also affect the layout of annotations.

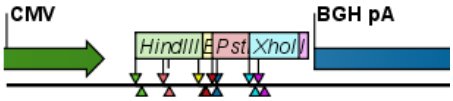


Figure 14.2: *Restriction site labels shown as flags.*

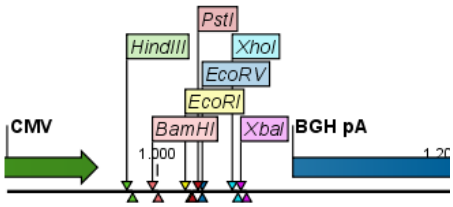


Figure 14.3: *Restriction site labels stacked.*

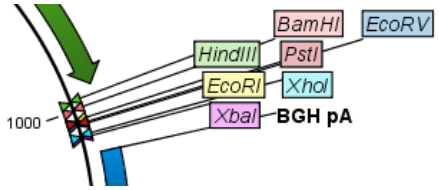


Figure 14.4: *Restriction site labels in radial layout.*

14.1.1 Sort enzymes

Just above the list of enzymes there are three buttons to be used for sorting the list (see figure 14.5):

Figure 14.5: *Buttons to sort restriction enzymes.*

- **Sort enzymes alphabetically** (). Clicking this button will sort the list of enzymes alphabetically.
- **Sort enzymes by number of restriction sites** (). This will divide the enzymes into four groups:
  - Non-cutters.
  - Single cutters.
  - Double cutters.
  - Multiple cutters.

  There is a checkbox for each group which can be used to hide / show all the enzymes in a group.
- **Sort enzymes by overhang** (). This will divide the enzymes into three groups:
  - Blunt. Enzymes cutting both strands at the same position.
  - 3'. Enzymes producing an overhang at the 3' end.
  - 5'. Enzymes producing an overhang at the 5' end.

  There is a checkbox for each group which can be used to hide / show all the enzymes in a group.

14.1.2 Manage enzymes

The list of restriction enzymes contains per default 20 of the most popular enzymes, but you can easily modify this list and add more enzymes by clicking the **Manage enzymes button.** This will display the dialog shown in figure 14.6.

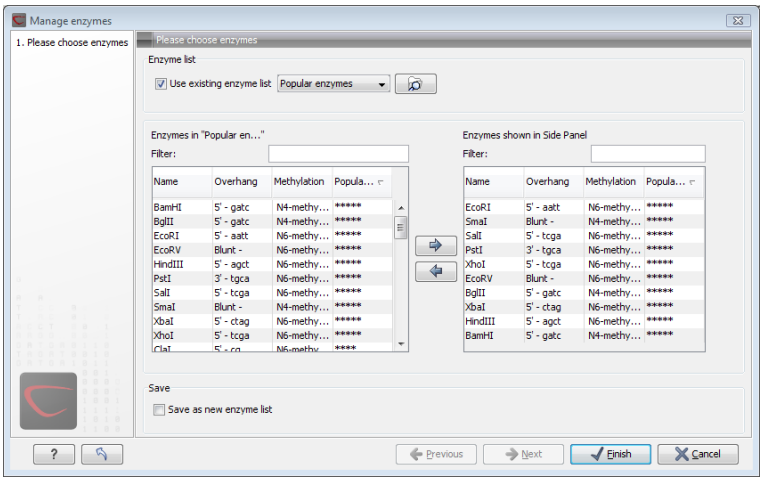


Figure 14.6: *Adding or removing enzymes from the Side Panel.*

At the top, you can choose to **Use existing enzyme list**. Clicking this option lets you select an enzyme list which is stored in the **Navigation Area**. See section 14.3 for more about creating and modifying enzyme lists.

Below there are two panels:

- To the **left**, you can see all the enzymes that are in the list selected above. If you have not chosen to use an existing enzyme list, this panel shows all the enzymes available [1].
- To the **right**, you can see the list of the enzymes that will be used.

Select enzymes in the left side panel and add them to the right panel by double-clicking or clicking the **Add** button (➡). If you e.g. wish to use EcoRV and BamHI, select these two enzymes and add them to the right side panel.

If you wish to use all the enzymes in the list:

Click in the panel to the left | press Ctrl + A (⌘ + A on Mac) | Add (➡)

The enzymes can be sorted by clicking the column headings, i.e. Name, Overhang, Methylation or Popularity. This is particularly useful if you wish to use enzymes which produce e.g. a 3' overhang. In this case, you can sort the list by clicking the Overhang column heading, and all the enzymes producing 3' overhangs will be listed together for easy selection.

When looking for a specific enzyme, it is easier to use the Filter. If you wish to find e.g. HindIII sites, simply type HindIII into the filter, and the list of enzymes will shrink automatically to only include the HindIII enzyme. This can also be used to only show enzymes producing e.g. a 3' overhang as shown in figure 14.17.

[1] The *CLC Sequence Viewer* comes with a standard set of enzymes based on http://rebase.neb.com/rebase/rebase.html. You can customize the enzyme database for your installation, see section D

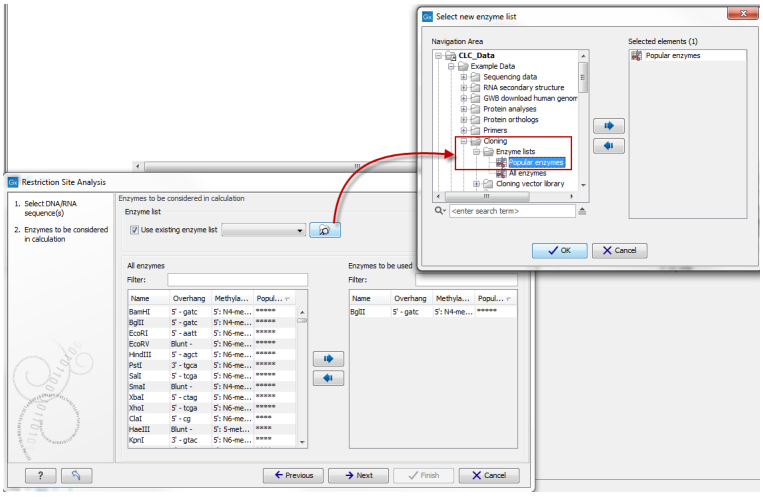


Figure 14.7: *Selecting enzymes.*

If you need more detailed information and filtering of the enzymes, either place your mouse cursor on an enzyme for one second to display additional information (see figure 14.18), or use the view of enzyme lists (see 14.3).

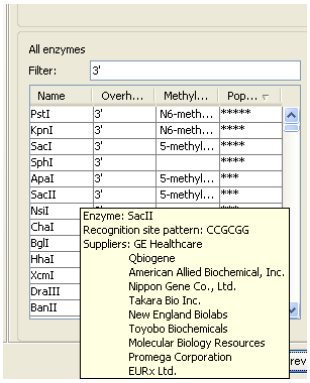


Figure 14.8: *Showing additional information about an enzyme like recognition sequence or a list of commercial vendors.*

At the bottom of the dialog, you can select to save this list of enzymes as a new file. In this way, you can save the selection of enzymes for later use.

When you click **Finish**, the enzymes are added to the Side Panel and the cut sites are shown on the sequence.

If you have specified a set of enzymes which you always use, it will probably be a good idea to save the settings in the Side Panel (see section 3.2.8) for future use.

14.2 Restriction site analysis from the Toolbox

Besides the dynamic restriction sites, you can do a more elaborate restriction map analysis with more output format using the Toolbox:

Toolbox | **Restriction Sites (** **)** | **Restriction Site Analysis (** **)**

This will display the dialog shown in figure 14.9.

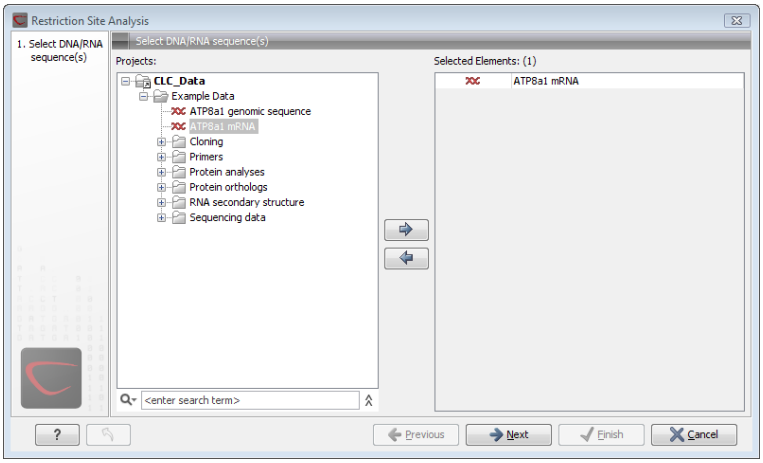


Figure 14.9: *Choosing sequence ATP8a1 mRNA for restriction map analysis.*

If a sequence was selected before choosing the Toolbox action, this sequence is now listed in the **Selected Elements** window of the dialog. Use the arrows to add or remove sequences or sequence lists from the selected elements.

14.2.1 Selecting, sorting and filtering enzymes

Clicking **Next** lets you define which enzymes to use as basis for finding restriction sites on the sequence. At the top, you can choose to **Use existing enzyme list**. Clicking this option lets you select an enzyme list which is stored in the **Navigation Area**. See section 14.3 for more about creating and modifying enzyme lists.

Below there are two panels:

- To the **left**, you can see all the enzymes that are in the list selected above. If you have not chosen to use an existing enzyme list, this panel shows all the enzymes available [2].
- To the **right**, you can see the list of the enzymes that will be used.

Select enzymes in the left side panel and add them to the right panel by double-clicking or clicking the **Add** button (➡). If you e.g. wish to use EcoRV and BamHI, select these two enzymes and add them to the right side panel.

If you wish to use all the enzymes in the list:

Click in the panel to the left | press Ctrl + A (⌘ + A on Mac) | Add (➡)

The enzymes can be sorted by clicking the column headings, i.e. Name, Overhang, Methylation or Popularity. This is particularly useful if you wish to use enzymes which produce e.g. a 3' overhang. In this case, you can sort the list by clicking the Overhang column heading, and all the enzymes producing 3' overhangs will be listed together for easy selection.

When looking for a specific enzyme, it is easier to use the Filter. If you wish to find e.g. HindIII sites, simply type HindIII into the filter, and the list of enzymes will shrink automatically to only include the HindIII enzyme. This can also be used to only show enzymes producing e.g. a 3' overhang as shown in figure 14.17.

[2] The *CLC Sequence Viewer* comes with a standard set of enzymes based on http://rebase.neb.com/rebase/

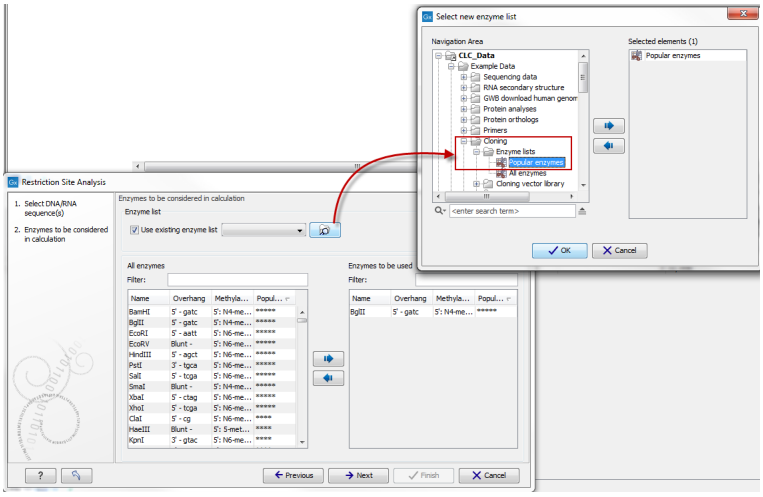


Figure 14.10: *Selecting enzymes.*

If you need more detailed information and filtering of the enzymes, either place your mouse cursor on an enzyme for one second to display additional information (see figure 14.18), or use the view of enzyme lists (see 14.3).

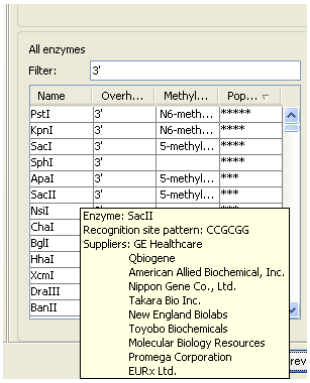


Figure 14.11: *Showing additional information about an enzyme like recognition sequence or a list of commercial vendors.*

14.2.2 Number of cut sites

Clicking **Next** confirms the list of enzymes which will be included in the analysis, and takes you to the dialog shown in figure 14.12.

If you wish the output of the restriction map analysis only to include restriction enzymes which cut the sequence a specific number of times, use the checkboxes in this dialog:

- No restriction site (**0**)
- One restriction site (**1**)
- Two restriction sites (**2**)
- Three restriction site (**3**)

`rebase.html`. You can customize the enzyme database for your installation, see section D

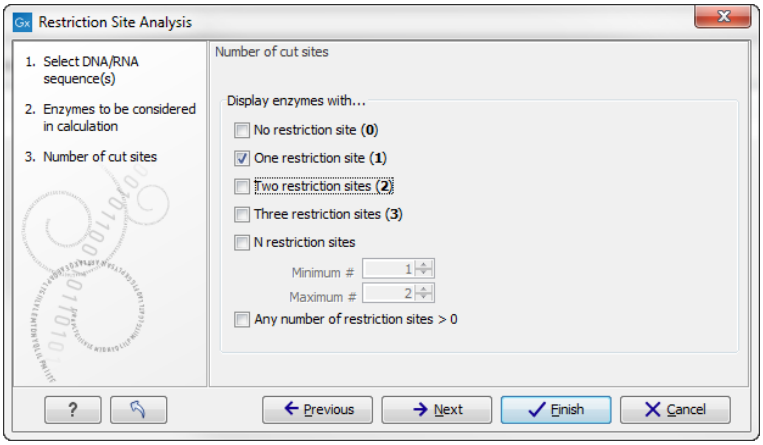


Figure 14.12: *Selecting number of cut sites.*

- N restriction sites
  - Minimum
  - Maximum
- Any number of restriction sites > 0

The default setting is to include the enzymes which cut the sequence one or two times.

You can use the checkboxes to perform very specific searches for restriction sites: e.g. if you wish to find enzymes which do not cut the sequence, or enzymes cutting exactly twice.

14.2.3 Output of restriction map analysis

Clicking next shows the dialog in figure 14.13.

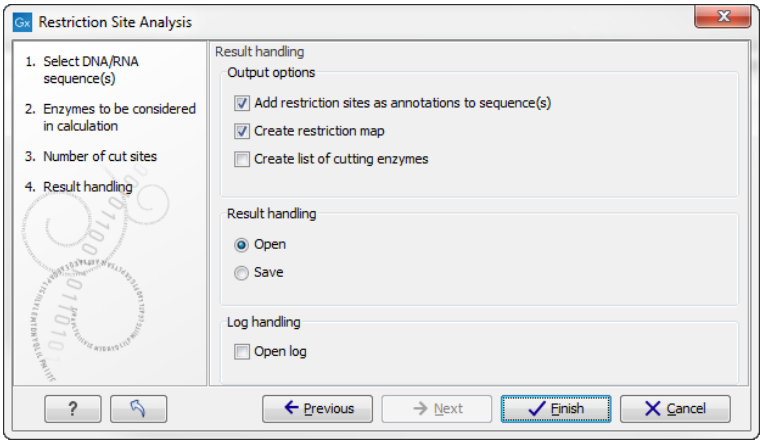


Figure 14.13: *Choosing to add restriction sites as annotations or creating a restriction map.*

This dialog lets you specify how the result of the restriction map analysis should be presented:

- **Add restriction sites as annotations to sequence(s)**. This option makes it possible to see the restriction sites on the sequence (see figure 14.14) and save the annotations for later use.

- **Create restriction map**. The restriction map is a table of restriction sites as shown in figure 14.15. If more than one sequence were selected, the table will include the restriction sites of all the sequences. This makes it easy to compare the result of the restriction map analysis for two sequences (or more).

The following sections will describe these output formats in more detail.

In order to complete the analysis click **Finish** (see section 8.1 for information about the Save and Open options).

14.2.4 Restriction sites as annotation on the sequence

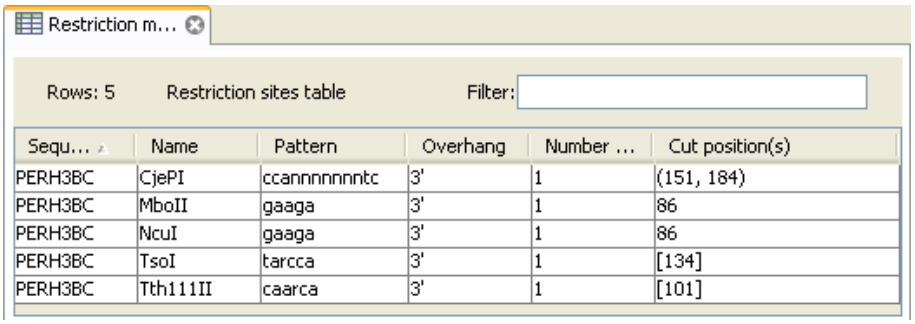
If you chose to add the restriction sites as annotation to the sequence, the result will be similar to the sequence shown in figure 14.14. See section 9.3 for more information about viewing

Figure 14.14: *The result of the restriction analysis shown as annotations.*

annotations.

14.2.5 Table of restriction sites

The restriction map can be shown as a table of restriction sites (see figure 14.15).



Sequ...	Name	Pattern	Overhang	Number ...	Cut position(s)
PERH3BC	CjePI	ccannnnnnntc	3'	1	(151, 184)
PERH3BC	MboII	gaaga	3'	1	86
PERH3BC	NcuI	gaaga	3'	1	86
PERH3BC	TsoI	tarcca	3'	1	[134]
PERH3BC	Tth111II	caarca	3'	1	[101]

Figure 14.15: *The result of the restriction analysis shown as annotations.*

Each row in the table represents a restriction enzyme. The following information is available for each enzyme:

- **Sequence**. The name of the sequence which is relevant if you have performed restriction map analysis on more than one sequence.
- **Name**. The name of the enzyme.
- **Pattern**. The recognition sequence of the enzyme.
- **Overhang**. The overhang produced by cutting with the enzyme (3', 5' or Blunt).
- **Number of cut sites**.

- **Cut position(s)**. The position of each cut.
  - **,** If the enzyme cuts more than once, the positions are separated by commas.
  - **[]** If the enzyme's recognition sequence is on the negative strand, the cut position is put in brackets (as the enzyme TsoI in figure 14.15 whose cut position is [134]).
  - **()** Some enzymes cut the sequence twice for each recognition site, and in this case the two cut positions are surrounded by parentheses.

14.3 Restriction enzyme lists

CLC Sequence Viewer includes all the restriction enzymes available in the **REBASE** database[3]. However, when performing restriction site analyses, it is often an advantage to use a customized list of enzymes. In this case, the user can create special lists containing e.g. all enzymes available in the laboratory freezer, all enzymes used to create a given restriction map or all enzymes that are available form the preferred vendor.

In the example data (see section 1.5.3) under Nucleotide->Restriction analysis, there are two enzyme lists: one with the 50 most popular enzymes, and another with all enzymes that are included in the *CLC Sequence Viewer*.

This section describes how you can create an enzyme list, and how you can modify it.

14.3.1 Create enzyme list

CLC Sequence Viewer uses enzymes from the **REBASE** restriction enzyme database at `http://rebase.neb.com`[4].

To create an enzyme list of a subset of these enzymes:

File | **New** | **Enzyme list (** **)**

This opens the dialog shown in figure 14.16

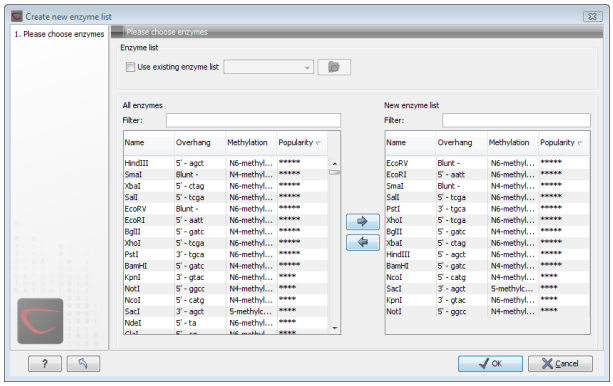


Figure 14.16: *Choosing enzymes for the new enzyme list.*

At the top, you can choose to **Use existing enzyme list**. Clicking this option lets you select an enzyme list which is stored in the **Navigation Area**. See section 14.3 for more about creating and modifying enzyme lists.

[3] You can customize the enzyme database for your installation, see section D
[4] You can customize the enzyme database for your installation, see section D

Below there are two panels:

- To the **left**, you can see all the enzymes that are in the list selected above. If you have not chosen to use an existing enzyme list, this panel shows all the enzymes available [5].
- To the **right**, you can see the list of the enzymes that will be used.

Select enzymes in the left side panel and add them to the right panel by double-clicking or clicking the **Add** button (➡). If you e.g. wish to use EcoRV and BamHI, select these two enzymes and add them to the right side panel.

If you wish to use all the enzymes in the list:

Click in the panel to the left | press Ctrl + A (⌘ + A on Mac) | Add (➡)

The enzymes can be sorted by clicking the column headings, i.e. Name, Overhang, Methylation or Popularity. This is particularly useful if you wish to use enzymes which produce e.g. a 3' overhang. In this case, you can sort the list by clicking the Overhang column heading, and all the enzymes producing 3' overhangs will be listed together for easy selection.

When looking for a specific enzyme, it is easier to use the Filter. If you wish to find e.g. HindIII sites, simply type HindIII into the filter, and the list of enzymes will shrink automatically to only include the HindIII enzyme. This can also be used to only show enzymes producing e.g. a 3' overhang as shown in figure 14.17.

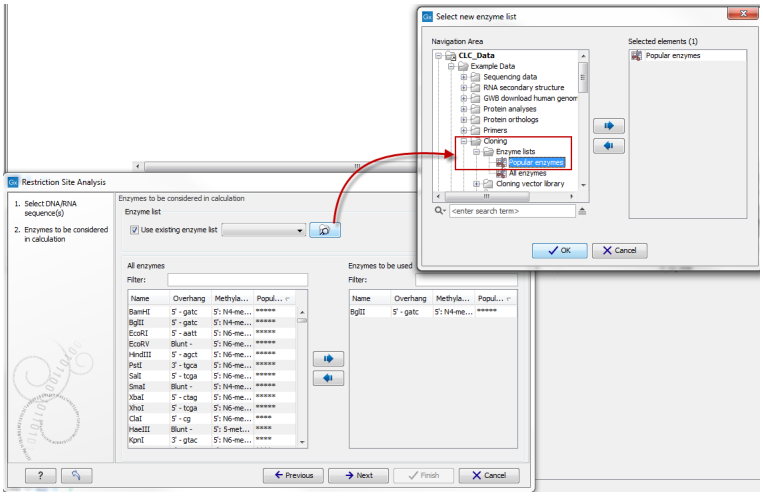


Figure 14.17: *Selecting enzymes.*

If you need more detailed information and filtering of the enzymes, either place your mouse cursor on an enzyme for one second to display additional information (see figure 14.18), or use the view of enzyme lists (see 14.3).

Click **Finish** to open the enzyme list.

14.3.2 View and modify enzyme list

An enzyme list is shown in figure 14.19. The list can be sorted by clicking the columns,

[5] The *CLC Sequence Viewer* comes with a standard set of enzymes based on http://rebase.neb.com/rebase/rebase.html. You can customize the enzyme database for your installation, see section D

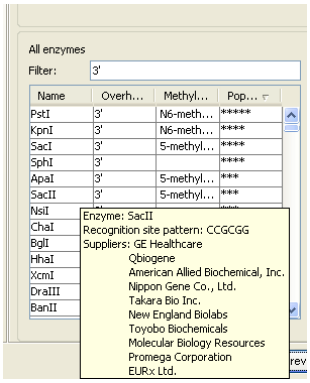


Figure 14.18: *Showing additional information about an enzyme like recognition sequence or a list of commercial vendors.*

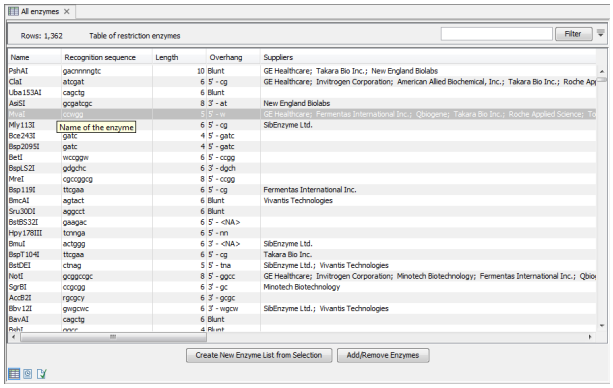


Figure 14.19: *An enzyme list.*

and you can use the filter at the top right corner to search for specific enzymes, recognition sequences etc.

If you wish to remove or add enzymes, click the **Add/Remove Enzymes** button at the bottom of the view. This will present the same dialog as shown in figure 14.16 with the enzyme list shown to the right.

If you wish to extract a subset of an enzyme list:

> **open the list** | **select the relevant enzymes** | **right-click** | **Create New Enzyme List from Selection** ( )

If you combined this method with the filter located at the top of the view, you can extract a very specific set of enzymes. E.g. if you wish to create a list of enzymes sold by a particular distributor, type the name of the distributor into the filter, and select and create a new enzyme list from the selection.

Chapter 15

Sequence alignment

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CLC Sequence Viewer can align nucleotides and proteins using a *progressive alignment* algorithm (see section 15.4 or read the White paper on alignments in the **Science** section of http://www.clcbio.com).
This chapter describes how to use the program to align sequences. The chapter also describes alignment algorithms in more general terms.

15.1 Create an alignment

To create an alignment in *CLC Sequence Viewer*:

Toolbox | **Alignments and Trees** ( )| **Create Alignment** ( )

This opens the dialog shown in figure 15.1.

If you have selected some elements before choosing the Toolbox action, they are now listed in the **Selected Elements** window of the dialog. Use the arrows to add or remove sequences, sequence lists or alignments from the selected elements. Click **Next** to adjust alignment algorithm parameters. Clicking **Next** opens the dialog shown in figure 15.2.

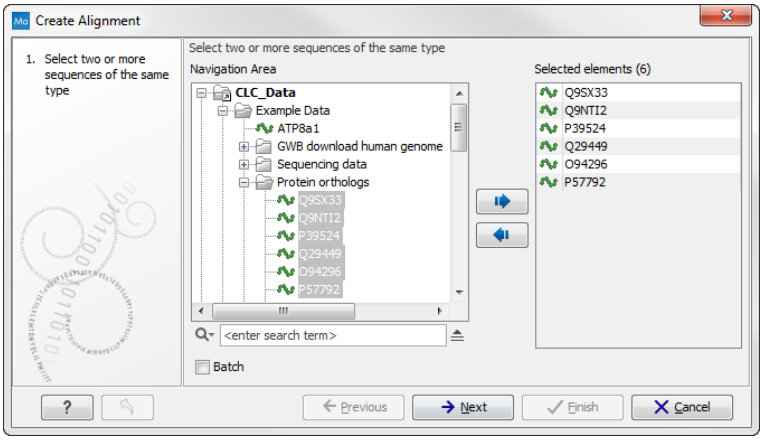

Figure 15.1: *Creating an alignment.*

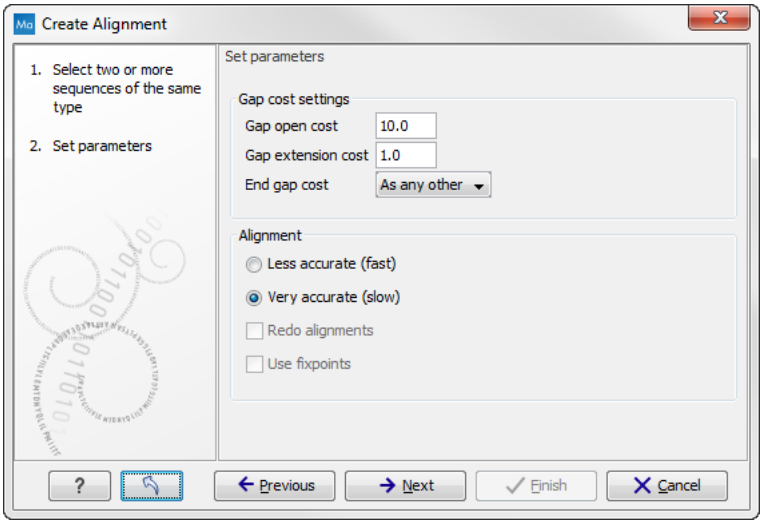

Figure 15.2: *Adjusting alignment algorithm parameters.*

15.1.1 Gap costs

The alignment algorithm has three parameters concerning gap costs: Gap open cost, Gap extension cost and End gap cost. The precision of these parameters is to one place of decimal.

- **Gap open cost**. The price for introducing gaps in an alignment.
- **Gap extension cost**. The price for every extension past the initial gap.

If you expect a lot of small gaps in your alignment, the Gap open cost should equal the Gap extension cost. On the other hand, if you expect few but large gaps, the Gap open cost should be set significantly higher than the Gap extension cost.

However, for most alignments it is a good idea to make the Gap open cost quite a bit higher than the Gap extension cost. The default values are 10.0 and 1.0 for the two parameters, respectively.

- **End gap cost**. The price of gaps at the beginning or the end of the alignment. One of the advantages of the *CLC Sequence Viewer* alignment method is that it provides flexibility in the treatment of gaps at the ends of the sequences. There are three possibilities:

- **Free end gaps**. Any number of gaps can be inserted in the ends of the sequences without any cost.
- **Cheap end gaps**. All end gaps are treated as gap extensions and any gaps past 10 are free.
- **End gaps as any other**. Gaps at the ends of sequences are treated like gaps in any other place in the sequences.

When aligning a long sequence with a short partial sequence, it is ideal to use free end gaps, since this will be the best approximation to the situation. The many gaps inserted at the ends are not due to evolutionary events, but rather to partial data.

Many homologous proteins have quite different ends, often with large insertions or deletions. This confuses alignment algorithms, but using the **Cheap end gaps** option, large gaps will generally be tolerated at the sequence ends, improving the overall alignment. This is the default setting of the algorithm.

Finally, treating end gaps like any other gaps is the best option when you know that there are no biologically distinct effects at the ends of the sequences.

Figures 15.3 and 15.4 illustrate the differences between the different gap scores at the sequence ends.

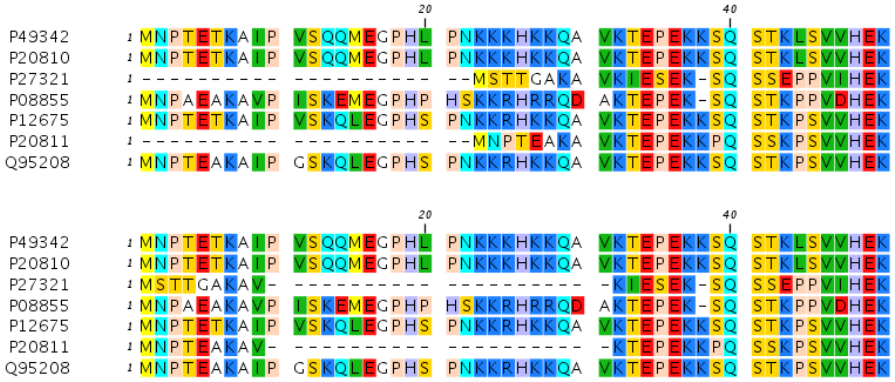
20
40
P49342 1 MNPTETKAIP VSQQMEGPHL PNKKKHKKQA VKTEPEKKSQ STKLSVVHEK
P20810 1 MNPTETKAIP VSQQMEGPHL PNKKKHKKQA VKTEPEKKSQ STKLSVVHEK
P27321 1 ---------- ---------- --MSTTGAKA VKIESEK-SQ SSEPPVIHEK
P08855 1 MNPAEAKAVP ISKEMEGPHP HSKKRHRRQD AKTEPEK-SQ STKPPVDHEK
P12675 1 MNPTETKAIP VSKQLEGPHS PNKKRHKKQA VKTEPEKKSQ STKPSVVHEK
P20811 1 ---------- ---------- --MNPTEAKA VKTEPEKKPQ SSKPSVVHEK
Q95208 1 MNPTEAKAIP GSKQLEGPHS PNKKRHKKQA VKTEPEKKSQ STKPSVVHEK
20
40
P49342 1 MNPTETKAIP VSQQMEGPHL PNKKKHKKQA VKTEPEKKSQ STKLSVVHEK
P20810 1 MNPTETKAIP VSQQMEGPHL PNKKKHKKQA VKTEPEKKSQ STKLSVVHEK
P27321 1 MSTTGAKAV- ---------- ---------- -KIESEK-SQ SSEPPVIHEK
P08855 1 MNPAEAKAVP ISKEMEGPHP HSKKRHRRQD AKTEPEK-SQ STKPPVDHEK
P12675 1 MNPTETKAIP VSKQLEGPHS PNKKRHKKQA VKTEPEKKSQ STKPSVVHEK
P20811 1 MNPTEAKAV- ---------- ---------- -KTEPEKKPQ SSKPSVVHEK
Q95208 1 MNPTEAKAIP GSKQLEGPHS PNKKRHKKQA VKTEPEKKSQ STKPSVVHEK

Figure 15.3: *The first 50 positions of two different alignments of seven calpastatin sequences. The top alignment is made with cheap end gaps, while the bottom alignment is made with end gaps having the same price as any other gaps. In this case it seems that the latter scoring scheme gives the best result.*

15.1.2 Fast or accurate alignment algorithm

CLC Sequence Viewer has two algorithms for calculating alignments:

- **Fast (less accurate).** This allows for use of an optimized alignment algorithm which is very fast. The fast option is particularly useful for data sets with very long sequences.
- **Slow (very accurate).** This is the recommended choice unless you find the processing time too long.

Both algorithms use progressive alignment. The faster algorithm builds the initial tree by doing more approximate pairwise alignments than the slower option.

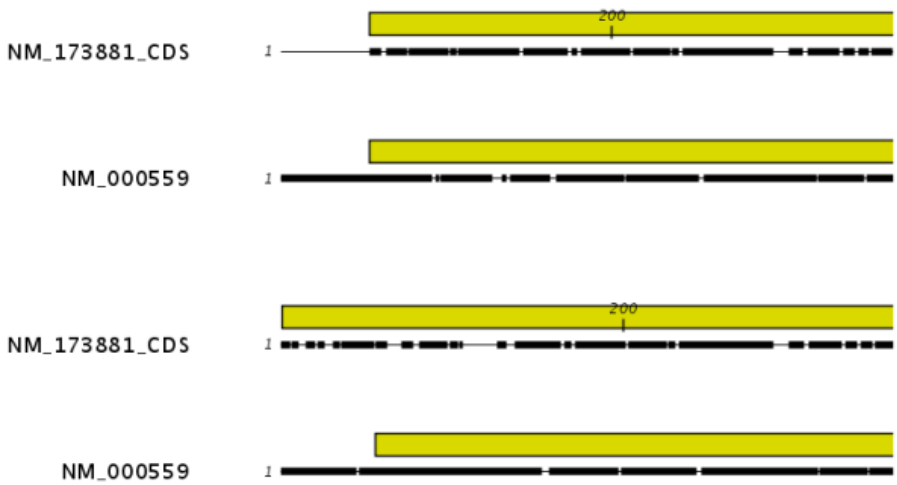

Figure 15.4: *The alignment of the coding sequence of bovine myoglobin with the full mRNA of human gamma globin. The top alignment is made with free end gaps, while the bottom alignment is made with end gaps treated as any other. The yellow annotation is the coding sequence in both sequences. It is evident that free end gaps are ideal in this situation as the start codons are aligned correctly in the top alignment. Treating end gaps as any other gaps in the case of aligning distant homologs where one sequence is partial leads to a spreading out of the short sequence as in the bottom alignment.*

15.2 View alignments

Since an alignment is a display of several sequences arranged in rows, the basic options for viewing alignments are the same as for viewing sequences. Therefore we refer to section 9.1 for an explanation of these basic options.

However, there are a number of alignment-specific view options in the **Alignment info** in the **Side Panel** to the right of the view. Below is more information on these view options.

The options in the **Alignment info** relate to each column in the alignment:

- **Consensus.** Shows a consensus sequence at the bottom of the alignment. The consensus sequence is based on every single position in the alignment and reflects an artificial sequence which resembles the sequence information of the alignment, but only as one single sequence. If all sequences of the alignment is 100% identical the consensus sequence will be identical to all sequences found in the alignment. If the sequences of the alignment differ the consensus sequence will reflect the most common sequences in the alignment. Parameters for adjusting the consensus sequences are described below.
  - **Limit.** This option determines how conserved the sequences must be in order to agree on a consensus. Here you can also choose **IUPAC** which will display the ambiguity code when there are differences between the sequences. E.g. an alignment with **A** and a **G** at the same position will display an **R** in the consensus line if the **IUPAC** option is selected. (The IUPAC codes can be found in section F and E.) Please note that the IUPAC codes are only available for nucleotide alignments.
  - **No gaps.** Checking this option will not show gaps in the consensus.
  - **Ambiguous symbol.** Select how ambiguities should be displayed in the consensus line (as **N**, **?**, *****, **.** or **-**). This option has no effect if **IUPAC** is selected in the **Limit** list

above.

The **Consensus Sequence** can be opened in a new view, simply by right-clicking the **Consensus Sequence** and click **Open Consensus in New View**.

- **Conservation.** Displays the level of conservation at each position in the alignment. The conservation shows the conservation of all sequence positions. The height of the bar, or the gradient of the color reflect how conserved that particular position is in the alignment. If one position is 100% conserved the bar will be shown in full height, and it is colored in the color specified at the right side of the gradient slider.
  - **Foreground color.** Colors the letters using a gradient, where the right side color is used for highly conserved positions and the left side color is used for positions that are less conserved.
  - **Background color.** Sets a background color of the residues using a gradient in the same way as described above.
  - **Graph.** Displays the conservation level as a graph at the bottom of the alignment. The bar (default view) show the conservation of all sequence positions. The height of the graph reflects how conserved that particular position is in the alignment. If one position is 100% conserved the graph will be shown in full height. Learn how to export the data behind the graph in section 6.4.
    - **Height.** Specifies the height of the graph.
    - **Type.** The type of the graph.
      - **Line plot.** Displays the graph as a line plot.
      - **Bar plot.** Displays the graph as a bar plot.
      - **Colors.** Displays the graph as a color bar using a gradient like the foreground and background colors.
    - **Color box.** Specifies the color of the graph for line and bar plots, and specifies a gradient for colors.
- **Gap fraction.** Which fraction of the sequences in the alignment that have gaps. The gap fraction is only relevant if there are gaps in the alignment.
  - **Foreground color.** Colors the letter using a gradient, where the left side color is used if there are relatively few gaps, and the right side color is used if there are relatively many gaps.
  - **Background color.** Sets a background color of the residues using a gradient in the same way as described above.
  - **Graph.** Displays the gap fraction as a graph at the bottom of the alignment (Learn how to export the data behind the graph in section 6.4).
    - **Height.** Specifies the height of the graph.
    - **Type.** The type of the graph.
      - **Line plot.** Displays the graph as a line plot.
      - **Bar plot.** Displays the graph as a line plot.
      - **Colors.** Displays the graph as a color bar using a gradient like the foreground and background colors.
    - **Color box.** Specifies the color of the graph for line and bar plots, and specifies a gradient for colors.

- **Color different residues.** Indicates differences in aligned residues.
  - **Foreground color.** Colors the letter.
  - **Background color.** Sets a background color of the residues.

15.3 Edit alignments

15.3.1 Move residues and gaps

The placement of gaps in the alignment can be changed by modifying the parameters when creating the alignment (see section 15.1). However, gaps and residues can also be moved after the alignment is created:

select one or more gaps or residues in the alignment | drag the selection to move

This can be done both for single sequences, but also for multiple sequences by making a selection covering more than one sequence. When you have made the selection, the mouse pointer turns into a horizontal arrow indicating that the selection can be moved (see figure 15.5).

Note! Residues can only be moved when they are next to a gap.

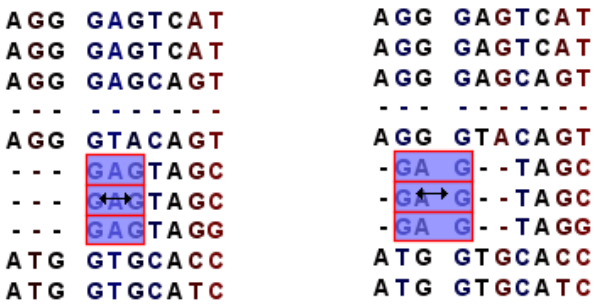

Figure 15.5: *Moving a part of an alignment. Notice the change of mouse pointer to a horizontal arrow.*

15.3.2 Insert gaps

The placement of gaps in the alignment can be changed by modifying the parameters when creating the alignment. However, gaps can also be added manually after the alignment is created.

To insert extra gaps:

select a part of the alignment | right-click the selection | Add gaps before/after

If you have made a selection covering e.g. five residues, a gap of five will be inserted. In this way you can easily control the number of gaps to insert. Gaps will be inserted in the sequences that you selected. If you make a selection in two sequences in an alignment, gaps will be inserted into these two sequences. This means that these two sequences will be displaced compared to the other sequences in the alignment.

15.3.3 Delete residues and gaps

Residues or gaps can be deleted for individual sequences or for the whole alignment. For individual sequences:

> **select the part of the sequence you want to delete** | **right-click the selection** | **Edit Selection (** **)** | **Delete the text in the dialog** | **Replace**

The selection shown in the dialog will be replaced by the text you enter. If you delete the text, the selection will be replaced by an empty text, i.e. deleted.

In order to delete entire columns:

> **manually select the columns to delete** | **right-click the selection** | **click 'Delete Selection'**

15.3.4 Move sequences up and down

Sequences can be moved up and down in the alignment:

> **drag the name of the sequence up or down**

When you move the mouse pointer over the label, the pointer will turn into a vertical arrow indicating that the sequence can be moved.

The sequences can also be sorted automatically to let you save time moving the sequences around. To sort the sequences alphabetically:

> **Right-click the name of a sequence** | **Sort Sequences Alphabetically**

If you change the Sequence name (in the **Sequence Layout** view preferences), you will have to ask the program to sort the sequences again.

If you have one particular sequence that you would like to use as a reference sequence, it can be useful to move this to the top. This can be done manually, but it can also be done automatically:

> **Right-click the name of a sequence** | **Move Sequence to Top**

15.3.5 Delete and rename sequences

Sequences can be removed from the alignment by right-clicking the label of a sequence:

> **right-click label** | **Delete Sequence**

This can be undone by clicking **Undo** ( ) in the Toolbar.

If you wish to delete several sequences, you can check all the sequences, right-click and choose **Delete Marked Sequences**. To show the checkboxes, you first have to click the **Show Selection Boxes** in the **Side Panel**.

A sequence can also be renamed:

> **right-click label** | **Rename Sequence**

This will show a dialog, letting you rename the sequence. This will not affect the sequence that

the alignment is based on.

15.4 Bioinformatics explained: Multiple alignments

Multiple alignments are at the core of bioinformatical analysis. Often the first step in a chain of bioinformatical analyses is to construct a multiple alignment of a number of homologs DNA or protein sequences. However, despite their frequent use, the development of multiple alignment algorithms remains one of the algorithmically most challenging areas in bioinformatical research.

Constructing a multiple alignment corresponds to developing a hypothesis of how a number of sequences have evolved through the processes of character substitution, insertion and deletion. The input to multiple alignment algorithms is a number of homologous sequences i.e. sequences that share a common ancestor and most often also share molecular function. The generated alignment is a table (see figure 15.6) where each row corresponds to an input sequence and each column corresponds to a position in the alignment. An individual column in this table represents residues that have all diverged from a common ancestral residue. Gaps in the table (commonly represented by a '-') represent positions where residues have been inserted or deleted and thus do not have ancestral counterparts in all sequences.

15.4.1 Use of multiple alignments

Once a multiple alignment is constructed it can form the basis for a number of analyses:

- The phylogenetic relationship of the sequences can be investigated by tree-building methods based on the alignment.
- Annotation of functional domains, which may only be known for a subset of the sequences, can be transferred to aligned positions in other un-annotated sequences.
- Conserved regions in the alignment can be found which are prime candidates for holding functionally important sites.
- Comparative bioinformatical analysis can be performed to identify functionally important regions.

15.4.2 Constructing multiple alignments

Whereas the optimal solution to the pairwise alignment problem can be found in reasonable time, the problem of constructing a multiple alignment is much harder.

The first major challenge in the multiple alignment procedure is how to rank different alignments i.e. which *scoring function* to use. Since the sequences have a shared history they are correlated through their *phylogeny* and the scoring function should ideally take this into account. Doing so is, however, not straightforward as it increases the number of model parameters considerably. It is therefore commonplace to either ignore this complication and assume sequences to be unrelated, or to use heuristic corrections for shared ancestry.

The second challenge is to find the optimal alignment given a scoring function. For pairs of sequences this can be done by *dynamic programming* algorithms, but for more than three sequences this approach demands too much computer time and memory to be feasible.

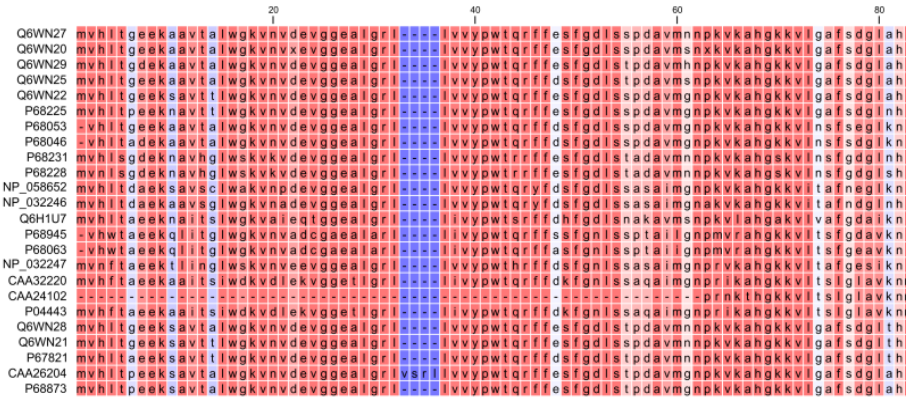

Figure 15.6: *The tabular format of a multiple alignment of 24 Hemoglobin protein sequences. Sequence names appear at the beginning of each row and the residue position is indicated by the numbers at the top of the alignment columns. The level of sequence conservation is shown on a color scale with blue residues being the least conserved and red residues being the most conserved.*

A commonly used approach is therefore to do *progressive alignment* [Feng and Doolittle, 1987] where multiple alignments are built through the successive construction of pairwise alignments. These algorithms provide a good compromise between time spent and the quality of the resulting alignment

Presently, the most exciting development in multiple alignment methodology is the construction of *statistical alignment* algorithms [Hein, 2001], [Hein et al., 2000]. These algorithms employ a scoring function which incorporates the underlying phylogeny and use an explicit stochastic model of molecular evolution which makes it possible to compare different solutions in a statistically rigorous way. The optimization step, however, still relies on dynamic programming and practical use of these algorithms thus awaits further developments.

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Chapter 16

Phylogenetic trees

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16.1 Phylogenetic tree features

Phylogenetics describes the taxonomical classification of organisms based on their evolutionary history i.e. their phylogeny. Phylogenetics is therefore an integral part of the science of systematics that aims to establish the phylogeny of organisms based on their characteristics. Furthermore, phylogenetics is central to evolutionary biology as a whole as it is the condensation of the overall paradigm of how life arose and developed on earth. The focus of this module is the reconstruction and visualization of phylogenetic trees. Phylogenetic trees illustrate the inferred evolutionary history of a set of organisms, and makes it possible to e.g. identify groups of closely related organisms and observe clustering of organisms with common traits. See 16.2.2 for a more detailed introduction to phylogenetic trees.

The viewer for visualizing and working with phylogenetic trees allows the user to create high-quality, publication-ready figures of phylogenetic trees. Large trees can be explored in two alternative tree layouts; circular and radial.

Below is an overview of the main features of the phylogenetic tree editor. Further details can be found in the subsequent sections.

Main features of the phylogenetic tree editor:

- Circular and radial layouts.
- Options for collapsing nodes based on bootstrap values.
- Re-ordering of tree nodes.
- Minimap navigation.
- Coloring and labeling of subtrees.
- Curved edges.
- Editable node sizes and line width.
- Intelligent visualization of overlapping labels and nodes.

16.2 Create Trees

For a given set of aligned sequences (see section 15.1) it is possible to infer their evolutionary relationships. In *CLC Sequence Viewer* this may be done using one of two distance based methods (see "Bioinformatics explained" in section 16.2.2).

16.2.1 Create tree

The "Create tree" tool can be used to generate a distance-based phylogenetic tree with multiple alignments as input:

Toolbox | **Alignments and Trees** ( )| **Create Tree** ( )

This will open the dialog displayed in figure 16.1:

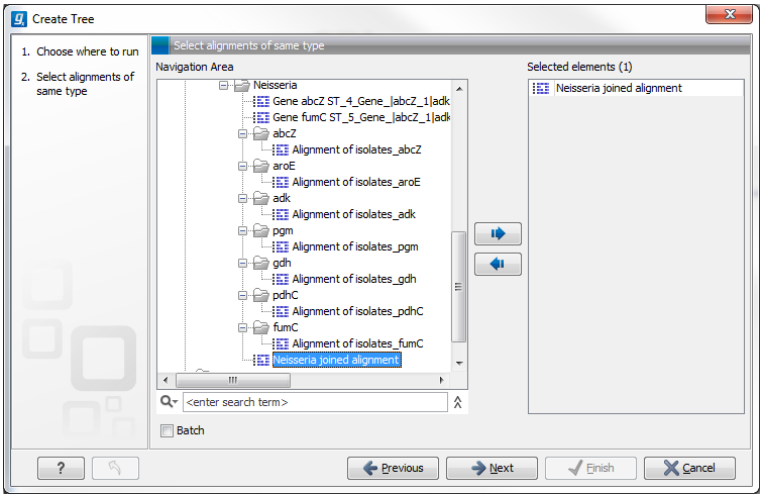

Figure 16.1: *Creating a tree.*

If an alignment was selected before choosing the Toolbox action, this alignment is now listed in the **Selected Elements** window of the dialog. Use the arrows to add or remove elements from the **Navigation Area**. Click **Next** to adjust parameters.

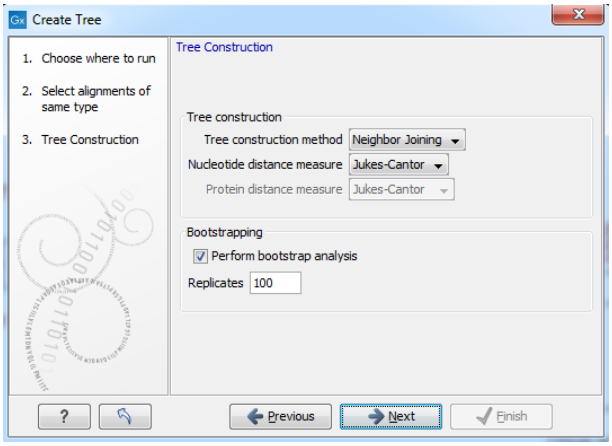

Figure 16.2: *Adjusting parameters for distance-based methods.*

Figure 16.2 shows the parameters that can be set for this distance-based tree creation:

- Tree construction (see section 16.2.2)
  - Tree construction method
    - The **UPGMA** method. Assumes constant rate of evolution.
    - The **Neighbor Joining** method. Well suited for trees with varying rates of evolution.
  - Nucleotide distance measure
    - **Jukes-Cantor**. Assumes equal base frequencies and equal substitution rates.
    - **Kimura 80**. Assumes equal base frequencies but distinguishes between transitions and transversions.
  - Protein distance measure
    - **Jukes-Cantor**. Assumes equal amino acid frequency and equal substitution rates.
    - **Kimura protein**. Assumes equal amino acid frequency and equal substitution rates. Includes a small correction term in the distance formula that is intended to give better distance estimates than Jukes-Cantor.
- Bootstrapping.
  - Perform bootstrap analysis. To evaluate the reliability of the inferred trees, *CLC Sequence Viewer* allows the option of doing a **bootstrap** analysis (see section 16.2.2). A bootstrap value will be attached to each node, and this value is a measure of the confidence in the subtree rooted at the node. The number of replicates used in the bootstrap analysis can be adjusted in the wizard. The default value is 100 replicates which is usually enough to distinguish between reliable and unreliable nodes in the tree. The bootstrap value assigned to each inner node in the output tree is the percentage (0-100) of replicates which contained the same subtree as the one rooted at the inner node.

For a more detailed explanation, see "Bioinformatics explained" in section 16.2.2.

16.2.2 Bioinformatics explained

The phylogenetic tree

The evolutionary hypothesis of a phylogeny can be graphically represented by a phylogenetic tree.

Figure 16.3 shows a proposed phylogeny for the great apes, *Hominidae*, taken in part from Purvis [Purvis, 1995]. The tree consists of a number of nodes (also termed vertices) and branches (also termed edges). These nodes can represent either an individual, a species, or a higher grouping and are thus broadly termed taxonomical units. In this case, the terminal nodes (also called leaves or tips of the tree) represent extant species of *Hominidae* and are the *operational taxonomical units* (OTUs). The internal nodes, which here represent extinct common ancestors of the great apes, are termed *hypothetical taxonomical units* since they are not directly observable.

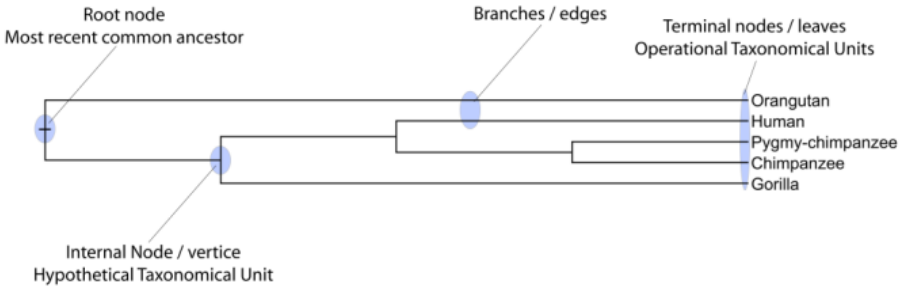

Figure 16.3: *A proposed phylogeny of the great apes (Hominidae). Different components of the tree are marked, see text for description.*

The ordering of the nodes determine the tree *topology* and describes how lineages have diverged over the course of evolution. The branches of the tree represent the amount of evolutionary divergence between two nodes in the tree and can be based on different measurements. A tree is completely specified by its topology and the set of all edge lengths.

The phylogenetic tree in figure 16.3 is rooted at the most recent common ancestor of all *Hominidae* species, and therefore represents a hypothesis of the direction of evolution e.g. that the common ancestor of gorilla, chimpanzee and man existed before the common ancestor of chimpanzee and man. In contrast, an unrooted tree would represent relationships without assumptions about ancestry.

Modern usage of phylogenies

Besides evolutionary biology and systematics the inference of phylogenies is central to other areas of research.

As more and more genetic diversity is being revealed through the completion of multiple genomes, an active area of research within bioinformatics is the development of comparative machine learning algorithms that can simultaneously process data from multiple species [Siepel and Haussler, 2004]. Through the comparative approach, valuable evolutionary information can be obtained about which amino acid substitutions are functionally tolerant to the organism and which are not. This information can be used to identify substitutions that affect protein function and stability, and is of major importance to the study of proteins [Knudsen and Miyamoto, 2001]. Knowledge of the underlying phylogeny is, however, paramount to comparative methods

of inference as the phylogeny describes the underlying correlation from shared history that exists between data from different species.

In molecular epidemiology of infectious diseases, phylogenetic inference is also an important tool. The very fast substitution rate of microorganisms, especially the RNA viruses, means that these show substantial genetic divergence over the time-scale of months and years. Therefore, the phylogenetic relationship between the pathogens from individuals in an epidemic can be resolved and contribute valuable epidemiological information about transmission chains and epidemiologically significant events [Leitner and Albert, 1999], [Forsberg et al., 2001].

Distance based reconstruction methods

Distance based phylogenetic reconstruction methods use a pairwise distance estimate between the input organisms to reconstruct trees. The distances are an estimate of the evolutionary distance between each pair of organisms which are usually computed from DNA or amino acid sequences. Given two homologous sequences a distance estimate can be computed by aligning the sequences and then counting the number of positions where the sequences differ. The number of differences is called the observed number of substitutions and is usually an underestimate of the real distance as multiple mutations could have occurred at any position.

To correct for these hidden substitutions a substitution model, such as Jukes-Cantor or Kimura 80, can be used to get a more precise distance estimate.

Alternatively, k-mer based methods or SNP based methods can be used to get a distance estimate without the use of substitution models.

After distance estimates have been computed, a phylogenetic tree can be reconstructed using a distance based reconstruction method. Most distance based methods perform a bottom up reconstruction using a greedy clustering algorithm. Initially, each input organism is put in its own cluster which corresponds to a leaf node in the resulting tree. Next, pairs of clusters are iteratively joined into higher level clusters, which correspond to connecting two nodes in the tree with a new parent node. When a single node remains, the tree is reconstructed.

The *CLC Sequence Viewer* provides two of the most widely used distance based reconstruction methods:

- The **UPGMA** method [Michener and Sokal, 1957] which assumes a constant rate of evolution (molecular clock hypothesis) in the different lineages. This method reconstruct trees by iteratively joining the two nearest clusters until there is only one cluster left. The result of the UPGMA method is a rooted bifurcating tree annotated with branch lengths.
- The **Neighbor Joining** method [Saitou and Nei, 1987] attempts to reconstruct a minimum evolution tree (a tree where the sum of all branch lengths is minimized). Opposite to the UPGMA method, the neighbor joining method is well suited for trees with varying rates of evolution in different lineages. A tree is reconstructed by iteratively joining clusters which are close to each other but at the same time far from all other clusters. The resulting tree is a bifurcating tree with branch lenghts. Since no particular biological hypothesis is made about the placement of the root in this method, the resulting tree is unrooted.

Bootstrap tests

Bootstrap tests [Felsenstein, 1985] is one of the most common ways to evaluate the reliability of the topology of a phylogenetic tree. In a bootstrap test, trees are evaluated using Efron's re-sampling technique [Efron, 1982], which samples nucleotides from the original set of sequences as follows:

Given an alignment of n sequences (rows) of length l (columns), we randomly choose l columns in the alignment with replacement and use them to create a new alignment. The new alignment has n rows and l columns just like the original alignment but it may contain duplicate columns and some columns in the original alignment may not be included in the new alignment. From this new alignment we reconstruct the corresponding tree and compare it to the original tree. For each subtree in the original tree we search for the same subtree in the new tree and add a score of one to the node at the root of the subtree if the subtree is present in the new tree. This procedure is repeated a number of times (usually around 100 times). The result is a counter for each interior node of the original tree, which indicate how likely it is to observe the exact same subtree when the input sequences are sampled. A bootstrap value is then computed for each interior node as the percentage of resampled trees that contained the same subtree as that rooted at the node.

Bootstrap values can be seen as a measure of how reliably we can reconstruct a tree, given the sequence data available. If all trees reconstructed from resampled sequence data have very different topologies, then most bootstrap values will be low, which is a strong indication that the topology of the original tree cannot be trusted.

Scale bar

The scale bar unit depends on the distance measure used and the tree construction algorithm used. The trees produced using the Maximum Likelihood Phylogeny tool has a very specific interpretation: A distance of x means that the expected number of substitutions/changes per nucleotide (amino acid for protein sequences) is x. i.e. if the distance between two taxa is 0.01, you expected a change in each nucleotide independently with probability 1 %. For the remaining algorithms, there is not as nice an interpretation. The distance depends on the weight given to different mutations as specified by the distance measure.

16.3 Tree Settings

The Tree Settings Side Panel found in the left side of the view area can be used to adjust the tree layout.

The preferred tree layout settings (user defined tree settings) can be saved and applied via the top right **Save Tree Settings** (figure 16.4). Settings can either be saved **For This Tree Only** or for all saved phylogenetic trees (**For Tree View in General**). The first option will save the layout of the tree for that tree only and it ensures that the layout is preserved even if it is exported and opened by a different user. The second option stores the layout globally in the Workbench and makes it available to other trees through the **Apply Saved Settings** option.

Tree Settings contains the following categories:

- Minimap

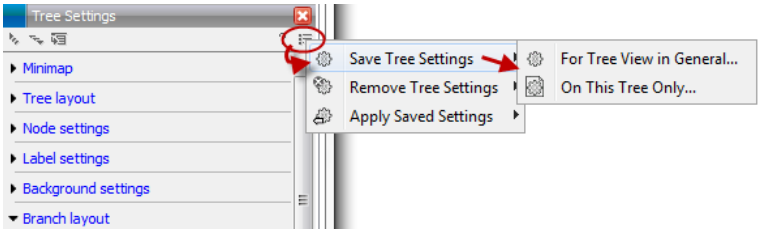

Figure 16.4: *Save, remove or apply preferred layout settings.*

- Tree layout
- Node settings
- Label settings
- Background settings
- Branch layout
- Bootstrap settings

16.3.1 Minimap

The Minimap is a navigation tool that shows a small version of the tree. A grey square indicates the specific part of the tree that is visible in the View Area (figure 16.5). To navigate the tree using the Minimap, click on the Minimap with the mouse and move the grey square around within the Minimap.

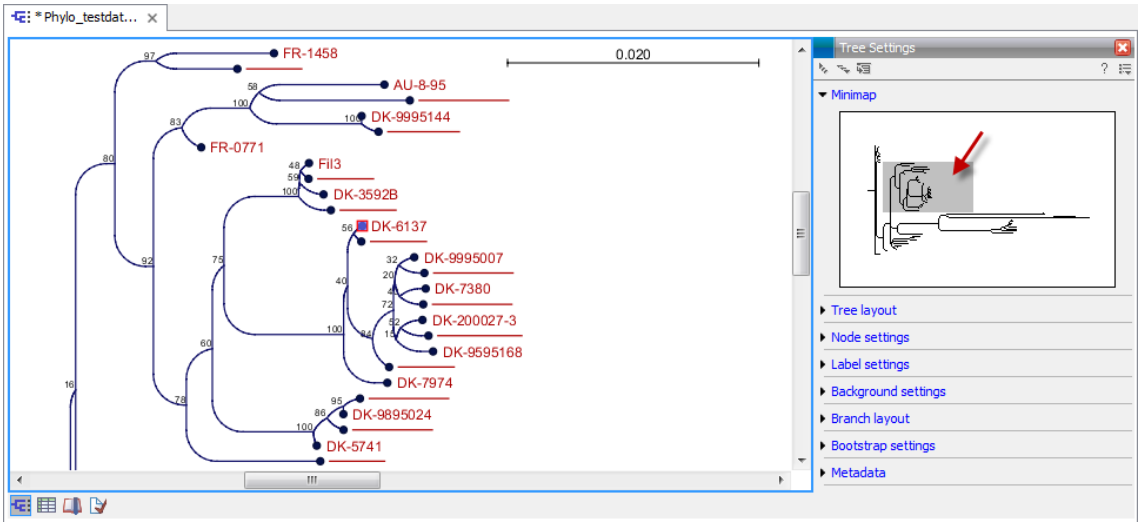

Figure 16.5: *Visualization of a phylogenetic tree. The grey square in the Minimap shows the part of the tree that is shown in the View Area.*

16.3.2 Tree layout

The **Tree Layout** can be adjusted in the Side Panel (figure 16.6).

- **Layout** Selects one of the five layout types: Phylogram, Cladogram, Circular Phylogram, Circular Cladogram or Radial. Note that only the Cladogram layouts are available if all branches in the tree have zero length.

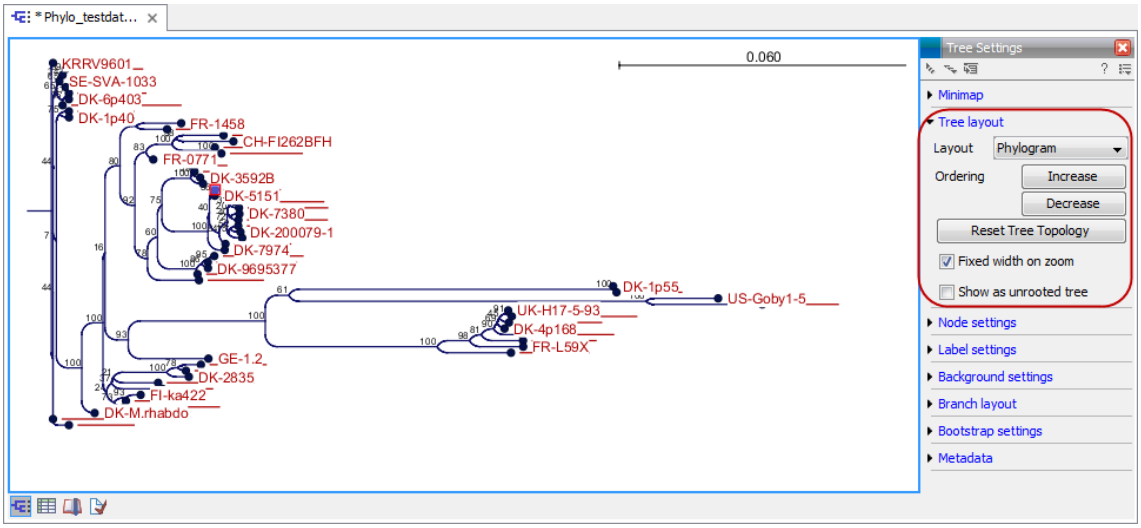

Figure 16.6: *The tree layout can be adjusted in the Side Panel. Five different layouts can be selected and the node order can be changed to increasing or decreasing. The tree topology and node order can be reverted to the original view with the button labeled "Reset Tree Topology".*

  - **Phylogram** is a rooted tree where the edges have "lengths", usually proportional to the inferred amount of evolutionary change to have occurred along each branch.
  - **Cladogram** is a rooted tree without branch lengths which is useful for visualizing the topology of trees.
  - **Circular Phylogram** is also a phylogram but with the leaves in a circular layout.
  - **Circular Cladogram** is also a cladogram but with the leaves in a circular layout.
  - **Radial** is an unrooted tree that has the same topology and branch lengths as the rooted styles, but lacks any indication of evolutionary direction.

- **Ordering** The nodes can be ordered after the branch length; either **Increasing** (shown in figure 16.7) or **Decreasing**.
- **Reset Tree Topology** Resets to the default tree topology and node order (see figure 16.7).
- **Ordering** The nodes can be ordered after the branch length; either **Increasing** (shown in figure 16.7) or **Decreasing**.
- **Reset Tree Topology** Resets to the default tree topology and node order (see figure 16.7).
- **Fixed width on zoom** Locks the horizontal size of the tree to the size of the main window. Zoom is therefore only performed on the vertical axis when this option is enabled.
- **Show as unrooted tree** The tree can be shown with or without a root.

16.3.3 Node settings

The nodes can be manipulated in several ways.

- **Leaf node symbol** Leaf nodes can be shown as a range of different symbols (Dot, Box, Circle, etc.).

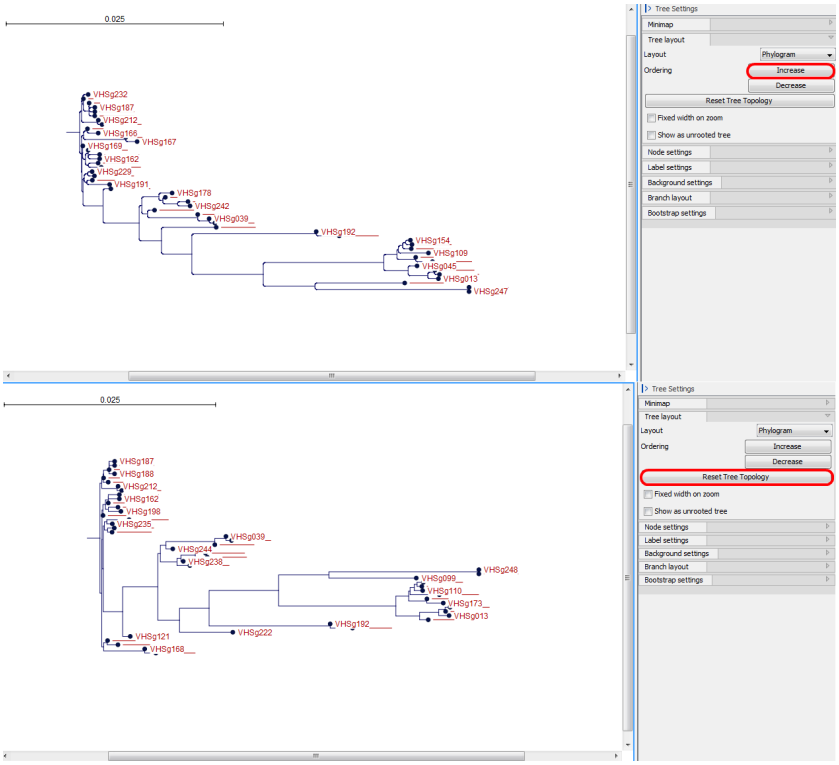

Figure 16.7: *The tree layout can be adjusted in the Side Panel. The top part of the figure shows a tree with increasing node order. In the bottom part of the figure the tree has been reverted to the original tree topology.*

- **Internal node symbols** The internal nodes can also be shown with a range of different symbols (Dot, Box, Circle, etc.).
- **Max. symbol size** The size of leaf- and internal node symbols can be adjusted.
- **Avoid overlapping symbols** The symbol size will be automatically limited to avoid overlaps between symbols in the current view.
- **Node color** Specify a fixed color for all nodes in the tree.

16.3.4 Label settings

- **Label font settings** Can be used to specify/adjust font type, size and typography (Bold, Italic or normal).
- **Hide overlapping labels** Disable automatic hiding of overlapping labels and display all labels even if they overlap.
- **Show internal node labels** Labels for internal nodes of the tree (if any) can be displayed. Please note that subtrees and nodes can be labeled with a custom text. This is done by right clicking the node and selecting **Edit Label** (see figure 16.8).
- **Show leaf node labels** Leaf node labels can be shown or hidden.
- **Rotate Subtree labels** Subtree labels can be shown horizontally or vertically. Labels are shown vertically when "Rotate subtree labels" has been selected. Subtree labels can

be added with the right click option "Set Subtree Label" that is enabled from "Decorate subtree" (see section 16.3.8).

- **Align labels** Align labels to the node furthest from the center of the tree so that all labels are positioned next to each other. The exact behavior depends on the selected tree layout.
- **Connect labels to nodes** Adds a thin line from the leaf node to the aligned label. Only possible when Align labels option is selected.

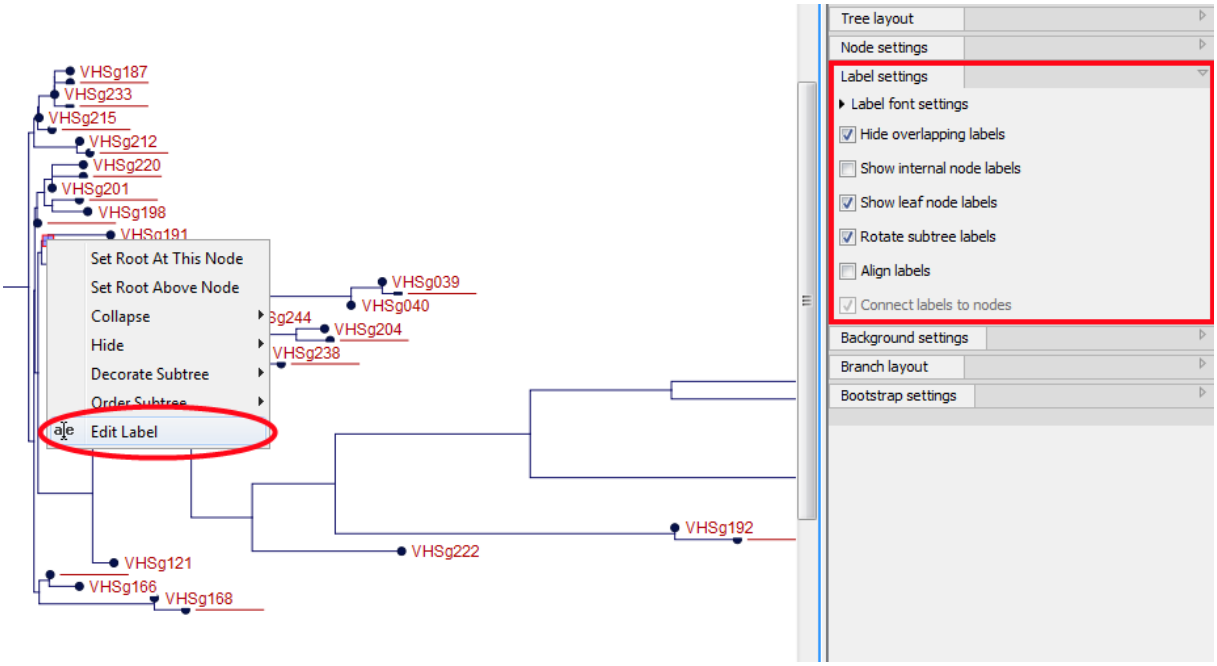

Figure 16.8: *"Edit label" in the right click menu can be used to customize the label text. The way node labels are displayed can be controlled through the labels settings in the right side panel.*

When working with big trees there is typically not enough space to show all labels. As illustrated in figure 16.8, only some of the labels are shown. The hidden labels are illustrated with thin horizontal lines (figure 16.9).

There are different ways of showing more labels. One way is to reduce the font size of the labels, which can be done under **Label font settings** in the Side Panel. Another option is to zoom in on specific areas of the tree (figure 16.9 and figure 16.10). The last option is to disable **Hide overlapping labels** under "Label settings" in the right side panel. When this option is unchecked all labels are shown even if the text overlaps. When allowing overlapping labels it is usually a good idea to disable **Show label background** under "Background settings" (see section 16.3.5).

Note! When working with a tree with hidden labels, it is possible to make the hidden label text appear by moving the mouse over the node with the hidden label.

16.3.5 Background settings

- **Show label background** Show a background color for each label. Once ticked, it is possible to specify a background color.

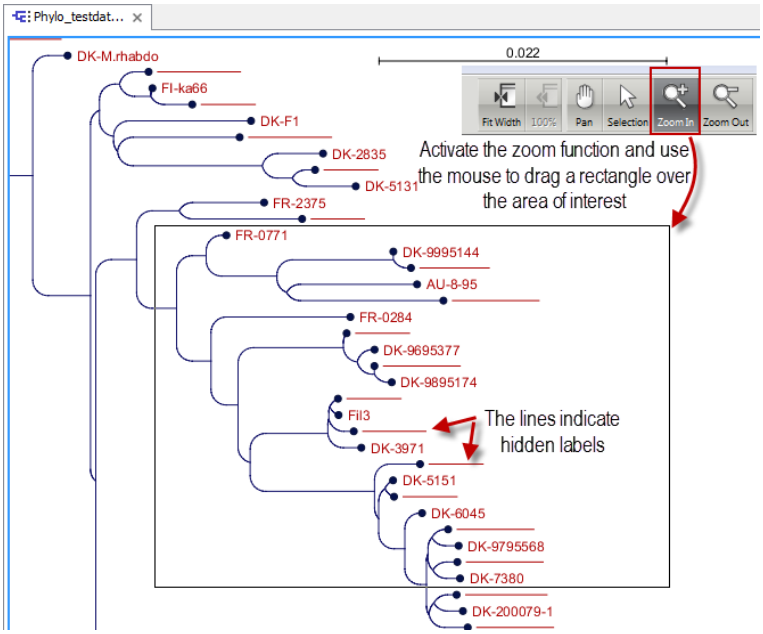

Figure 16.9: *The zoom function in the upper right corner of CLC Genomics Workbench can be used to zoom in on a particular region of the tree. When the zoom function has been activated, use the mouse to drag a rectangle over the area that you wish to zoom in at.*

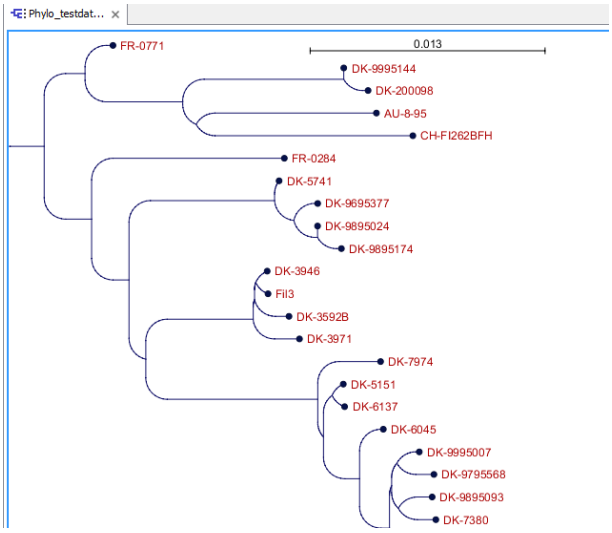

Figure 16.10: *After zooming in on a region of interest more labels become visible. In this example all labels are now visible.*

16.3.6 Branch layout

- **Branch length font settings** Specify/adjust font type, size and typography (Bold, Italic or normal).
- **Line color** Select the default line color.
- **Line width** Select the width of branches (1.0-3.0 pixels).
- **Curvature** Adjust the degree of branch curvature to get branches with round corners.
- **Min. length** Select a minimum branch length. This option can be used to prevent nodes connected with a short branch to cluster at the parent node.

- **Show branch lengths** Show or hide the branch lengths.

The branch layout settings in the Side Panel are shown in figure 16.11.

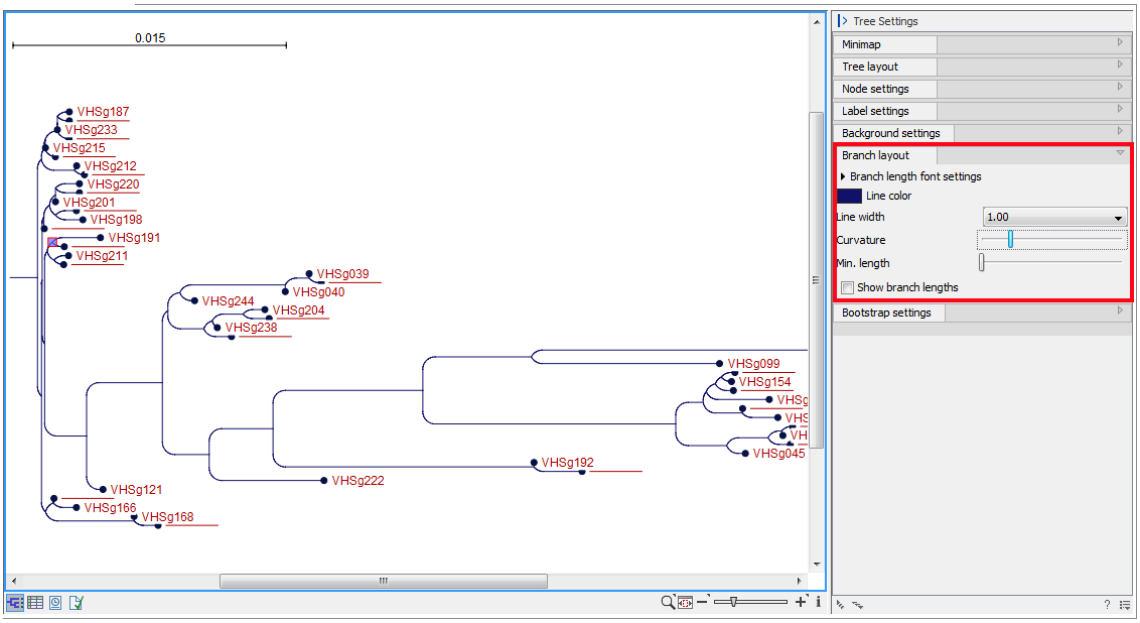

Figure 16.11: *Branch Layout settings.*

16.3.7 Bootstrap settings

Bootstrap values can be shown on the internal nodes. The bootstrap values are shown in percent and can be interpreted as confidence levels where a bootstrap value close to 100 indicate a clade, which is strongly supported by the data from which the tree was reconstructed. Bootstrap values are useful for identifying clades in the tree where the topology (and branch lengths) should not be trusted.

Some branches in rooted trees may not have bootstrap values. Trees constructed with neighbour joining are unrooted and to correctly visualize them, the "Radial" view is required. In all other tree views we need a root to visualize the tree. An "artificial node" and therefore an extra branch are created for such visualization to achieve this, which makes it look like a bootstrap value is missing

- **Bootstrap value font settings** Specify/adjust font type, size and typography (Bold, Italic or normal).
- **Show bootstrap values (%)** Show or hide bootstrap values. When selected, the bootstrap values (in percent) will be displayed on internal nodes if these have been computed during the reconstruction of the tree.
- **Bootstrap threshold (%)** When specifying a bootstrap threshold, the branch lengths can be controlled manually by collapsing internal nodes with bootstrap values under a certain threshold.
- **Highlight bootstrap $\geq$ (%)** Highlights branches where the bootstrap value is above the user defined threshold.

16.3.8 Node right click menu

Additional options for layout and extraction of subtree data are available when right clicking the nodes (figure 16.8):

Figure 16.12: *A subtree can be hidden by selecting "Hide Subtree" and is shown again when selecting "Show Hidden Subtree" on a parent node.*

- **Set Root At This Node** Re-root the tree using the selected node as root. Please note that re-rooting will change the tree topology.
- **Set Root Above Node** Re-root the tree by inserting a node between the selected node and its parent. Useful for rooting trees using an outgroup.
- **Collapse** Branches associated with a selected node can be collapsed with or without the associated labels. Collapsed branches can be uncollapsed using the *Uncollapse* option in the same menu.
- **Hide** Can be used to hide a node or a subtree. Hidden nodes or subtrees can be shown again using the *Show Hidden Subtree* function on a node which is root in a subtree

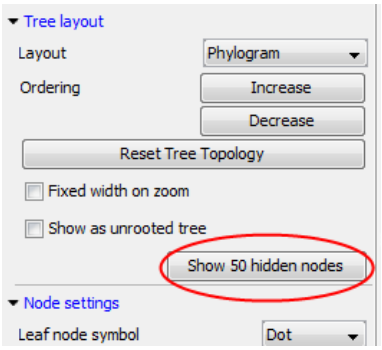

Figure 16.13: *When hiding nodes, a new button labeled "Show X hidden nodes" appears in the Side Panel under "Tree Layout". When pressing this button, all hidden nodes are brought back.*

containing hidden nodes (see figure 16.12). When hiding nodes, a new button appears labeled "Show X hidden nodes" in the Side Panel under "Tree Layout" (figure 16.13). When pressing this button, all hidden nodes are shown again.

- **Decorate Subtree** A subtree can be labeled with a customized name, and the subtree lines and/or background can be colored. To save the decoration, see figure 16.4 and use option: **Save/Restore Settings** | **Save Tree View Settings On This Tree View only**.
- **Order Subtree** Rearrange leaves and branches in a subtree by Increasing/Decreasing depth, respectively. Alternatively, change the order of a node's children by left clicking and dragging one of the node's children.
- **Edit label** Edit the text in the selected node label. Labels can be shown or hidden by using the Side Panel: **Label settings | Show internal node labels**

Part IV

Appendix

Appendix A

More features

You are currently using CLC bio's Sequence Viewer. If you want more features, try one of our commercial workbenches. You can download a one-month demo at http://www.clcbio.com/software.

See a list of all the features available below.

- CLC Sequence Viewer (■)
- CLC Main Workbench (■)
- CLC Genomics Workbench (■)

Data handling	Viewer	Main	Genomics
Add multiple locations to Navigation Area		■	■
Share data on network drive		■	■
Search all your data		■	■

Assembly of sequencing data	Viewer	Main	Genomics
Advanced contig assembly		■	■
Importing and viewing trace data		■	■
Trim sequences		■	■
Assemble without use of reference sequence		■	■
Map to reference sequence		■	■
Assemble to existing contig		■	■
Viewing and edit contigs		■	■
Tabular view of an assembled contig (easy data overview)		■	■
Secondary peak calling		■	■
Multiplexing based on barcode or name		■	■

Next-generation Sequencing Data Analysis	Viewer	Main	Genomics
Import of 454, Illumina Genome Analyzer, SOLiD and Helicos data			■
Reference assembly of human-size genomes			■
De novo assembly			■
SNP/DIP detection			■
Graphical display of large contigs			■
Support for mixed-data assembly			■
Paired data support			■
RNA-Seq analysis			■
Expression profiling by tags			■
ChIP-Seq analysis			■

Expression Analysis	Viewer	Main	Genomics
Import of Illumina BeadChip, Affymetrix, GEO data		■	■
Import of Gene Ontology annotation files		■	■
Import of Custom expression data table and Custom annotation files		■	■
Multigroup comparisons		■	■
Advanced plots: scatter plot, volcano plot, box plot and MA plot		■	■
Hierarchical clustering		■	■
Statistical analysis on count-based and gaussian data		■	■
Annotation tests		■	■
Principal component analysis (PCA)		■	■
Hierarchical clustering and heat maps		■	■
Analysis of RNA-Seq/Tag profiling samples		■	■

Molecular cloning	Viewer	Main	Genomics
Advanced molecular cloning		■	■
Graphical display of in silico cloning		■	■
Advanced sequence manipulation		■	■

Database searches	Viewer	Main	Genomics
GenBank Entrez searches	■	■	■
UniProt searches (Swiss-Prot/TrEMBL)		■	■
Web-based sequence search using BLAST		■	■
BLAST on local database		■	■
Creation of local BLAST database		■	■
PubMed lookup		■	■
Web-based lookup of sequence data		■	■
Search for structures (at NCBI)		■	■

General sequence analyses	Viewer	Main	Genomics
Linear sequence view	■	■	■
Circular sequence view	■	■	■
Text based sequence view		■	■
Editing sequences	■	■	■
Adding and editing sequence annotations		■	■
Advanced annotation table		■	■
Join multiple sequences into one	■	■	■
Sequence statistics	■	■	■
Shuffle sequence	■	■	■
Local complexity region analyses		■	■
Advanced protein statistics		■	■
Comprehensive protein characteristics report		■	■

Nucleotide analyses	Viewer	Main	Genomics
Basic gene finding	■	■	■
Reverse complement without loss of annotation	■	■	■
Restriction site analysis	■	■	■
Advanced interactive restriction site analysis		■	■
Translation of sequences from DNA to proteins	■	■	■
Interactive translations of sequences and alignments		■	■
G/C content analyses and graphs		■	■

Protein analyses	Viewer	Main	Genomics
3D molecule view		■	■
Hydrophobicity analyses		■	■
Antigenicity analysis		■	■
Protein charge analysis		■	■
Reverse translation from protein to DNA		■	■
Proteolytic cleavage detection		■	■
Prediction of signal peptides (SignalP)		■	■
Transmembrane helix prediction (TMHMM)		■	■
Secondary protein structure prediction		■	■
PFAM domain search		■	■

Sequence alignment	Viewer	Main	Genomics
Multiple sequence alignments (Two algorithms)	■	■	■
Advanced re-alignment and fix-point alignment options		■	■
Advanced alignment editing options	■	■	■
Join multiple alignments into one		■	■
Consensus sequence determination and management	■	■	■
Conservation score along sequences	■	■	■
Sequence logo graphs along alignments		■	■
Gap fraction graphs		■	■
Copy annotations between sequences in alignments		■	■
Pairwise comparison	■	■	■

RNA secondary structure	Viewer	Main	Genomics
Advanced prediction of RNA secondary structure		■	■
Integrated use of base pairing constraints		■	■
Graphical view and editing of secondary structure		■	■
Info about energy contributions of structure elements		■	■
Prediction of multiple sub-optimal structures		■	■
Evaluate structure hypothesis		■	■
Structure scanning		■	■
Partition function		■	■

Dot plots	Viewer	Main	Genomics
Dot plot based analyses		■	■

Phylogenetic trees	Viewer	Main	Genomics
Neighbor-joining and UPGMA phylogenies	■	■	■
Maximum likelihood phylogeny of nucleotides		■	■

Pattern discovery	Viewer	Main	Genomics
Search for sequence match	■	■	■
Motif search for basic patterns		■	■
Motif search with regular expressions		■	■
Motif search with ProSite patterns		■	■
Pattern discovery		■	■

Primer design	Viewer	Main	Genomics
Advanced primer design tools		■	■
Detailed primer and probe parameters		■	■
Graphical display of primers		■	■
Generation of primer design output		■	■
Support for Standard PCR		■	■
Support for Nested PCR		■	■
Support for TaqMan PCR		■	■
Support for Sequencing primers		■	■
Alignment based primer design		■	■
Alignment based TaqMan probe design		■	■
Match primer with sequence		■	■
Ordering of primers		■	■
Advanced analysis of primer properties		■	■

Molecular cloning	Viewer	Main	Genomics
Advanced molecular cloning		■	■
Graphical display of in silico cloning		■	■
Advanced sequence manipulation		■	■

Virtual gel view	Viewer	Main	Genomics
Fully integrated virtual 1D DNA gel simulator		■	■

Appendix B

Graph preferences

This section explains the view settings of graphs. The **Graph preferences** at the top of the **Side Panel** includes the following settings:

- **Lock axes.** This will always show the axes even though the plot is zoomed to a detailed level.
- **Frame.** Shows a frame around the graph.
- **Show legends.** Shows the data legends.
- **Tick type**. Determine whether tick lines should be shown outside or inside the frame.
  - Outside
  - Inside
- **Tick lines at.** Choosing Major ticks will show a grid behind the graph.
  - None
  - Major ticks
- **Horizontal axis range**. Sets the range of the horizontal axis (x axis). Enter a value in **Min** and **Max**, and press Enter. This will update the view. If you wait a few seconds without pressing Enter, the view will also be updated.
- **Vertical axis range**. Sets the range of the vertical axis (y axis). Enter a value in **Min** and **Max**, and press Enter. This will update the view. If you wait a few seconds without pressing Enter, the view will also be updated.
- **X-axis at zero**. This will draw the x axis at y = 0. Note that the axis range will not be changed.
- **Y-axis at zero**. This will draw the y axis at x = 0. Note that the axis range will not be changed.
- **Show as histogram**. For some data-series it is possible to see the graph as a histogram rather than a line plot.

The **Lines and plots** below contains the following settings:

- **Dot type**
  - None
  - Cross
  - Plus
  - Square
  - Diamond
  - Circle
  - Triangle
  - Reverse triangle
  - Dot
- **Dot color.** Allows you to choose between many different colors. Click the color box to select a color.
- **Line width**
  - Thin
  - Medium
  - Wide
- **Line type**
  - None
  - Line
  - Long dash
  - Short dash
- **Line color.** Allows you to choose between many different colors. Click the color box to select a color.

For graphs with multiple data series, you can select which curve the dot and line preferences should apply to. This setting is at the top of the **Side Panel** group.

Note that the graph title and the axes titles can be edited simply by clicking with the mouse. These changes will be saved when you **Save** ( ) the graph - whereas the changes in the **Side Panel** need to be saved explicitly (see section 4.5).

Appendix C

Formats for import and export

C.1 List of bioinformatic data formats

Below is a list of bioinformatic data formats, i.e. formats for importing and exporting molecule structures, sequences, alignments and trees.

C.1.1 Sequence data formats

File type	Suffix	Import	Export	Description
AB1	.ab1	X		Including chromatograms
ABI	.abi	X		Including chromatograms
CLC	.clc	X	X	Rich format including all information
Clone manager	.cm5	X		Clone manager sequence format
DNAstrider	.str/.strider	X	X	
DS Gene	.bsml	X		
EMBL	.emb/.embl	X	X	Rich information incl. annotations (nucs only)
FASTA	.fsa/.fasta	X	X	Simple format, name & description
GCG sequence	.gcg	X		Rich information incl. annotations
GenBank	.gbk/.gb/.gp	X	X	Rich information incl. annotations
Gene Construction Kit	.gck	X		
Lasergene	.pro/.seq	X		
Nexus	.nxs/.nexus	X	X	
Phred	.phd	X		Including chromatograms
PIR (NBRF)	.pir	X		Simple format, name & description
Raw sequence	any	X		Only sequence (no name)
SCF2	.scf	X		Including chromatograms
SCF3	.scf	X	X	Including chromatograms
Sequence Comma separated values	.csv	X	X	Simple format. One seq per line: name, description(optional), sequence
Staden	.sdn	X		
Swiss-Prot	.swp	X	X	Rich information incl. annotations (only peptides)
Tab delimited text	.txt		X	Annotations in tab delimited text format
Vector NTI archives*	.ma4/.pa4/.oa4	X		Archives in rich format
Vector NTI Database*		X		Special import full database

*Vector NTI import functionality comes as standard within the CLC Main Workbench and can be installed as a plugin via the Plugins Manager of the CLC Genomics Workbench (read more in section 1.6.1).

C.1.2 Alignment formats

File type	Suffix	Import	Export	Description
Aligned fasta	.fa	X	X	Simple fasta-based format with – for gaps
CLC	.clc	X	X	Rich format including all information
ClustalW	.aln	X	X	
GCG Alignment	.msf	X	X	
Nexus	.nxs/.nexus	X	X	
Phylip Alignment	.phy	X	X	

C.1.3 Tree formats

File type	Suffix	Import	Export	Description
CLC	.clc	X	X	Rich format including all information
Newick	.nwk	X	X	
Nexus	.nxs/.nexus	X	X	

C.1.4 Other formats

File type	Suffix	Import	Export	Description
CLC	.clc	X	X	Rich format including all information
PDB	.pdb	X		3D structure

C.1.5 Table and text formats

File type	Suffix	Import	Export	Description
Excel	.xls/.xlsx	X	X	All tables and reports
Table CSV	.csv	X	X	All tables
Tab delimited	.txt		X	All tables
Text	.txt	X	X	All data in a textual format
CLC	.clc	X	X	Rich format including all information
HTML	.html		X	All tables
PDF	.pdf		X	Export reports in Portable Document Format

C.1.6 File compression formats

File type	Suffix	Import	Export	Description
Zip export	.zip		X	Selected files in CLC format
Zip import	.zip/.gz/.tar	X		Contained files/folder structure

Note! It is possible to import 'external' files into the Workbench and view these in the **Navigation Area**, but it is only the above mentioned formats whose *contents* can be shown in the Workbench.

C.2 List of graphics data formats

Below is a list of formats for exporting graphics. All data displayed in a graphical format can be exported using these formats. Data represented in lists and tables can only be exported in .pdf

format (see section 6.3 for further details).

Format	Suffix	Type
Portable Network Graphics	.png	bitmap
JPEG	.jpg	bitmap
Tagged Image File	.tif	bitmap
PostScript	.ps	vector graphics
Encapsulated PostScript	.eps	vector graphics
Portable Document Format	.pdf	vector graphics
Scalable Vector Graphics	.svg	vector graphics

Appendix D

Restriction enzymes database configuration

CLC Sequence Viewer uses enzymes from the **REBASE** restriction enzyme database at http://rebase.neb.com. If you wish to add enzymes to this list, you can do this by manually using the procedure described here.

Note! Please be aware that this process needs to be handled carefully, otherwise you may have to re-install the Workbench to get it to work.

First, download the following file: http://www.clcbio.com/wbsettings/link_emboss_e_custom. In the Workbench installation folder under `settings`, create a folder named `rebase` and place the extracted `link_emboss_e_custom` file here.

Note that in MAC OS X, the extension file "link_emboss_e_custom" will have a ".txt" extension in its filename and metadata that needs to be removed. Right click the file name, choose "Get info" and remove ".txt" from the "Name & extension" field.

Open the file in a text editor. The top of the file contains information about the format, and at the bottom there are two example enzymes that you should replace with your own.

Please note that the CLC Workbenches only support the addition of 2-cutter enzymes. Further details about how to format your entries accordingly are given within the file mentioned above.

After adding the above file, or making changes to it, you must restart the Workbench for changes take effect.

Appendix E

IUPAC codes for amino acids

(Single-letter codes based on International Union of Pure and Applied Chemistry)

The information is gathered from: http://www.insdc.org/documents/feature_table.html

One-letter abbreviation	Three-letter abbreviation	Description
A	Ala	Alanine
R	Arg	Arginine
N	Asn	Asparagine
D	Asp	Aspartic acid
C	Cys	Cysteine
Q	Gln	Glutamine
E	Glu	Glutamic acid
G	Gly	Glycine
H	His	Histidine
J	Xle	Leucine or Isoleucineucine
L	Leu	Leucine
I	ILe	Isoleucine
K	Lys	Lysine
M	Met	Methionine
F	Phe	Phenylalanine
P	Pro	Proline
O	Pyl	Pyrrolysine
U	Sec	Selenocysteine
S	Ser	Serine
T	Thr	Threonine
W	Trp	Tryptophan
Y	Tyr	Tyrosine
V	Val	Valine
B	Asx	Aspartic acid or Asparagine Asparagine
Z	Glx	Glutamic acid or Glutamine Glutamine
X	Xaa	Any amino acid

Appendix F

IUPAC codes for nucleotides

(Single-letter codes based on International Union of Pure and Applied Chemistry)

The information is gathered from: http://www.iupac.org and http://www.insdc.org/documents/feature_table.html.

Code	Description
A	Adenine
C	Cytosine
G	Guanine
T	Thymine
U	Uracil
R	Purine (A or G)
Y	Pyrimidine (C, T, or U)
M	C or A
K	T, U, or G
W	T, U, or A
S	C or G
B	C, T, U, or G (not A)
D	A, T, U, or G (not C)
H	A, T, U, or C (not G)
V	A, C, or G (not T, not U)
N	Any base (A, C, G, T, or U)

Bibliography

[Andrade et al., 1998] Andrade, M. A., O'Donoghue, S. I., and Rost, B. (1998). Adaptation of protein surfaces to subcellular location. *J Mol Biol*, 276(2):517–525.

[Bachmair et al., 1986] Bachmair, A., Finley, D., and Varshavsky, A. (1986). In vivo half-life of a protein is a function of its amino-terminal residue. *Science*, 234(4773):179–186.

[Clote et al., 2005] Clote, P., Ferré, F., Kranakis, E., and Krizanc, D. (2005). Structural RNA has lower folding energy than random RNA of the same dinucleotide frequency. *RNA*, 11(5):578–591.

[Efron, 1982] Efron, B. (1982). *The jackknife, the bootstrap and other resampling plans*, volume 38. SIAM.

[Felsenstein, 1985] Felsenstein, J. (1985). Confidence limits on phylogenies: An approach using the bootstrap. *Journal of Molecular Evolution*, 39:783–791.

[Feng and Doolittle, 1987] Feng, D. F. and Doolittle, R. F. (1987). Progressive sequence alignment as a prerequisite to correct phylogenetic trees. *J Mol Evol*, 25(4):351–360.

[Forsberg et al., 2001] Forsberg, R., Oleksiewicz, M. B., Petersen, A. M., Hein, J., Bøtner, A., and Storgaard, T. (2001). A molecular clock dates the common ancestor of European-type porcine reproductive and respiratory syndrome virus at more than 10 years before the emergence of disease. *Virology*, 289(2):174–179.

[Gill and von Hippel, 1989] Gill, S. C. and von Hippel, P. H. (1989). Calculation of protein extinction coefficients from amino acid sequence data. *Anal Biochem*, 182(2):319–326.

[Gonda et al., 1989] Gonda, D. K., Bachmair, A., Wünning, I., Tobias, J. W., Lane, W. S., and Varshavsky, A. (1989). Universality and structure of the N-end rule. *J Biol Chem*, 264(28):16700–16712.

[Hein, 2001] Hein, J. (2001). An algorithm for statistical alignment of sequences related by a binary tree. In *Pacific Symposium on Biocomputing*, page 179.

[Hein et al., 2000] Hein, J., Wiuf, C., Knudsen, B., Møller, M. B., and Wibling, G. (2000). Statistical alignment: computational properties, homology testing and goodness-of-fit. *J Mol Biol*, 302(1):265–279.

[Ikai, 1980] Ikai, A. (1980). Thermostability and aliphatic index of globular proteins. *J Biochem (Tokyo)*, 88(6):1895–1898.

[Knudsen and Miyamoto, 2001] Knudsen, B. and Miyamoto, M. M. (2001). A likelihood ratio test for evolutionary rate shifts and functional divergence among proteins. *Proc Natl Acad Sci U S A*, 98(25):14512–14517.

[Leitner and Albert, 1999] Leitner, T. and Albert, J. (1999). The molecular clock of HIV-1 unveiled through analysis of a known transmission history. *Proc Natl Acad Sci U S A*, 96(19):10752–10757.

[Michener and Sokal, 1957] Michener, C. and Sokal, R. (1957). A quantitative approach to a problem in classification. *Evolution*, 11:130–162.

[Purvis, 1995] Purvis, A. (1995). A composite estimate of primate phylogeny. *Philos Trans R Soc Lond B Biol Sci*, 348(1326):405–421.

[Saitou and Nei, 1987] Saitou, N. and Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol Biol Evol*, 4(4):406–425.

[Siepel and Haussler, 2004] Siepel, A. and Haussler, D. (2004). Combining phylogenetic and hidden Markov models in biosequence analysis. *J Comput Biol*, 11(2-3):413–428.

[Tobias et al., 1991] Tobias, J. W., Shrader, T. E., Rocap, G., and Varshavsky, A. (1991). The N-end rule in bacteria. *Science*, 254(5036):1374–1377.

Part V

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